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Minimum DB seq
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Perfect score:
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 200.6
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100.0 135751
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Match Length DB
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Listing first 45 summaries
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HSDJ81D8
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AC084862 Papio anu
AC084863 Papio anu
AC027197 Homo sapi
DD181590 LIPID-ASS
X06290 Human mRNA
AC093405 Lemur cat
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AC027197 Homo sapi
M34272 Human plasm
AY192161 Homo sapi
AL109933 Human DNA
AX815991 Sequence
AX463624 Sequence
AX815990 Sequence
AX815989 Sequence
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ALIGNMENTS

REFERENCE AUTHORS TITLE ACCESSION VERSION KEYWORDS RESULT 1 AL596089/c SOURCE COMMENT DEFINITION JOURNAL ORGANISM Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, all submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, all submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: vega@sanger.ac.uk Clone requestes: clonerequest@sanger.ac.uk
Clone requestes: clonerequest@sanger.ac.uk
Clone requestes: clonerequest@sanger.ac.uk
Clone requestes: used to associate primary accession rumbers given in the feature table with their source databases:
Em: SMB1; Sw: SWISSPROT; Tr:, TREMB1; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
RP11-414A5 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see AL596089 135751 bp DNA linear PRI 18-MAY-200 Human DNA sequence from clone RP11-414A5 on chromosome 6 Contains the 3' end of the LPA gene for lipoprotein (Lp(a)) and a CpG HTG; apolipoprotein; CpG island; kringle; lipoprotein; LPA. Homo sapiens (human) Web site: http://www.sanger.ac.uk http://www.chori.org/bacpac/home.htm VECTOR: pBACe3.6 Sycamore, N. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Center code: SC Center: Wellcome Trust Sanger Institute Hominidae; AL596089.19 GI:21425227 island, complete sequence. Homo sapiens (bases 1 to 135751) Genome Center linear PRI 18-MAY-2005

This sequence was finished as follows unless otherwise noted: all

FEATURES

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mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (12931.13912), complement (12854.128723), complement (12931.13912), complement (12854.128723), complement (12931.13916), complement (123017.123176), complement (124384.119021), complement (117470.117629), complement (113291.119021), complement (111924.112083), complement (10747.119028), complement (106380.106539), complement (10201.102201.102382), complement (10834.100993), complement (92201.102201.102382), complement (9279.95438), complement (90194.9015), complement (83217.83376), complement (84634.84815), complement (83217.83376), complement (84634.84815), complement (83217.83376), complement (70166.70347), complement (7075.703429), complement (70166.70347), complement (60853.68022), complement (70166.70347), complement (60853.68022), complement (2107.41288), complement (39742.39901), complement (22195.32376), complement (23195.3276), complement 
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                                                                                                                                  . .15272,21657.
.26525,29157.
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.29195))
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GYRGKKATTVTGTPCQEWAAQEPHRHSTFIPGTNKWAGLEKNYCRNPDGDINGPWCYT
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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT
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Birren,B., Linton,L., Nusbaum,C.
Homo sapiens chromosome 6, clone
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Mammalia; Eutheria;
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restriction digest data."
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Coske, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Ferreira, P., Firzhugh, M., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Lamazares, R., Landers, T., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McCheeters, R., Meldrim, J., McCarthy, M., McEwan, P., McKernan, K., Morrow, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, T., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rieback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Turavers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Ninger, A., and Zody, M.
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Aug 24, 2000 this sequence version replaced gi:9799792. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (28-MAR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA (Dases 1 to 194321)
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Center: Whitehead Institute/ MIT Center for Genome Research Web site: http://www-seq.wi.mit.edu Center code: WIBR --- Genome Center

Center project name: L7625 Center clone name: 189_0_14 Contact: sequence submissions@genome.wi.mit.edu

* NOTE: This record contains 224 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low-pass sequence sampling is useful for

* identifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that

* the record is updated, the accession number will

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                                                               Original source text: Homo sapiens DNA.

Draft entry and computer-readable sequence for [1] kindly submitted by A.Ichinose, 26-MAR-1990, for release after publication.
                                                                                             Petersen,T.E., Martzen,M.R., Ichinose,A.
Characterization of the gene for human pl
in the fibrinolytic system
J. Biol. Chem. 265 (11), 6104-6111 (1990)
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8328 9173 9173 9173 9173 9173 10021 11084 112408 112508 112508 114096 1140

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106 753
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100 bp

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9 0

gap of contig

100 bp of 691 100 bp of 741 100 bp of 722

gap conti

100 bp of 744 100 bp of 739

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gap c gap of contig gap of contig gap of contig gap c

100 bp of 730 100 bp of 747 100 bp of 730

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variation	variation	variation	variation	variation	× 5	variation	variation	variation	variation	variation	variacion	3	variation	variation	variation		variation	variation		variation	variation	Variation		variation	variation	9		variation	variation	variation
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PACLPSPNYVVADRTECFITGWGETGGTFGAGLLKEAQLPVISKKVCNYEFFLNGRVQ
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PACLPSPNYVVADRTECFITGWGETGGTFGAGLLKEAQLPVISKKVCNYEFFLNGRVQ
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FVTWIEGVMRNN"
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frequency="0.49"
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                                                                  replace="a"
                                                                                                                                                                                                                                          frequency="0.05"
replace="c"
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                                                                                                                  gene="PLG"
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AUTHORS
TITLE
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      Center: Wellcome Trust Sanger Institute Center code: SC
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                                                                                                                                                                                                                                                                                                                                                                            Tracey, A.
                                                                                                                                                                                                                                                                                                                                                                                                 Hominidae; Homo.
1 (bases I to 163599)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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3017. .6100
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rpt_type=dispersed
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39282 TrGACATCTCATCTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG
                                                                                         61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
                                                                                                                                                                1 TTGACATCCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG
                                                                     CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Region not scanned 3244. .3401
                                                                                                                                                                                                                    Score 187.8; DB 5; Pred. No. 3.7e-47; 1; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for variation"
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39461
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                                                                       39401
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HSDJ81D8
HSDJ81D8
HSDJ81D8
HUMAN DNA sequence from clone RPI-81D8 on chromosome 6q25.3-26
Contains the PLG gene for plasminogen, the 5' end of the LPA gene
for lipoprotein (Lp(a)), a novel gene, a pseudogene similar to par
of plasminogen and a CpG island, complete sequence.
AL109933
AL109933.25 GI:11344445
HTG; apolipoprotein; CpG; kringle; lipoprotein; LPA; plasminogen; PRI 18-MAY-2005

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries: vega@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Nov 25, 2000 this sequence version replaced gi:11322966. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 found at http://www.sanger.ac.uk/HGP/Chr6

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FEATURES
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Except on the rare occasion of the clone being a YAC.

RPI-81D8 is from the library RPCI-1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
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                                                                                                                                                                                                                                                                      Complement (AL596089.19:106380.10639), complement (AL596089.19:100834.100933), complement (AL596089.19:100834.100993), complement (AL596089.19:96649.96830), complement (AL596089.19:96649.96830), complement (AL596089.19:9673.88922), complement (AL596089.19:88763.88922), complement (AL596089.19:88763.88922), complement (AL596089.19:83317.83376), complement (AL596089.19:83317.77834), complement (AL596089.19:7675.77834), complement (AL596089.19:77675.77834), complement (AL596089.19:77675.77834), complement (AL596089.19:73270.73429), complement (AL596089.19:73270.73429), complement (AL596089.19:73270.73429), complement (AL596089.19:60763.62421), complement (AL596089.19:60853.61012), complement (AL596089.19:60853.61012), complement (AL596089.19:33166.7634), complement (AL596089.19:33166.7634), complement (AL596089.19:33166.76364), complement (AL596089.19:33166.76364), complement (AL596089.19:33166.76364), complement (AL596089.19:32157.29250), complement (AL596089.19:32157.2
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complement(AL596089.19:15200. .130112))
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match: cDNAs: X06290.1"
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/mol_type="genomic DNA"
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lement (AL596089.19:111924. .112083)
lement (AL596089.19:107747. .107928)
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.14180), complement (304.
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DPSTEASSEEAPTEOSPGVODCYHGDGOSYRGSFSTTVTGRTCOSWSSMTPHWHORTT
EYYPNGGLTRNYCRNPDAEISPWCYTMDPNVRWEYCNLTQCPVTESSVLATSTAVSEQ
APTEOSPTVQDCYHGDGQSYRGSFSTTVTGRTCOSWSSMTPHWHQRTTEYYPNGGLTR
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mplement (AL596089.19:102201. 102382),
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mplement (AL596089.19:95279. 95438),
mplement (AL596089.19:90194. 90375),
mplement (AL596089.19:88763. 88922),
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lement (AL596089.19:117924. .107928)
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.19:83217. .83376),
.19:79071. .79252),
.19:77675. .77834),
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19:41107.
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19:62240.
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Best Local
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Center: Washington University Genome Sequencing Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                           2 (bases 1 to 177878)

Waterston, R.H.

Direct Submission
Submitted (25-SEP-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Porest Park Parkway, St. MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:6850583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACO10893 177878 bp DNA linear H
Homo mapiens chromosome 6 clone RP11-480A20, WORKING
SEQUENCE, 18 unordered pieces.
ACO10893
ACO10893.5 GI:8568869
ACO10893.5 GI:8568869
                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 177878)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                              unpublished
                                                                                                                                                                                                                                                                                                                                         The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                              Hominidae; Homo.
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Similarity 95.0%;
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PVVRQCYHGNGGSYRGTFSTTVTGRTCGSWSSWTPHHARTPEXP
DADTGPWCFFWDPSIRWEYCNLTRCSDTEGTVVARPTVIQVPSLGPBESDCWEGNSK
GYRGKKATTVTGTPCQEWAAQEPHRHSTFIFGTNKWAGLEKNYCRNEDGDINGPWCYT
MNPRKLFDYCDLFLCASSSFDCGKPQVEFKKCPGSIVIGGCVAHHSWPWQVSLFRRFG
KHFCGGTLISPEWVLTAAHCLKKSRFSSYKVLIGAHOBVNLESHVQEIEVSRLFLES
TQADIALLKLSRPAVITDKVMPACLPSPDYMVTARTECYITGMGETQGTFGTGLLKEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(16194. .16339,26376. .26489))
/locus tag="RRP1-01D8.4-001"
/notes="match: proteins: 010783 046507 P00747 P06867 P06868
P12545 P20918 P80009 P80010 P81286 Q15146 Q29485 Q91WJ5
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/locus_tag="RP1-81D8.4-001"
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PNKPGVYARVSRFVTWIEGMWRNN"
                                                                                                Genome Center -----
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Pred. No. 1.1e-46;
1; Mismatches 9
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G DRAFT
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SOURCE

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Chemistry: Dye-primer ET; 76% of reads
Chemistry: Dye-terminator Big Dye; 24% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 165387 bases at least Q40
Consensus quality: 170279 bases at least Q30
Consensus quality: 170279 bases at least Q30
Consensus quality: 172646 bases at least Q20
Insert size: 183000; agarose-fp
Insert size: 183100; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 4.11 in Q20 bases; agarose-fp Quality coverage: 4.01 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: M13;
Sequencing vector: plasm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project name: H_NH0480A20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as soon as it is available be preserved.
                                                                                                                                                                                                                                               145034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7450
                                                                                                                                     /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="6"
                          /note="assembly_name:Contig41"
                                                            estimated/
                                                                                      /notes assembly_name: Contig28"
                                                                                                                                                                                                                ocation,
estimated_length=unknown)
                                                                                                                        clone="RP11-480A20"
                                                                                                                                                                                                                             116472: gap of unknown length
144933: contig of 28461 bp in
145033: gap of unknown length
177878: contig of 32845 bp in
                                                                                                                                                                                                                                                                         116372: contig
116472: gap of
                                                                                                                                                                                                                                                                                                             93897:
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                                                                                                                                                                                                                                                                                          1: contig of 6772 bp in length
1: gap of unknown length
6: contig of 7935 bp in length
7: contig of 1911 bp in length
7: contig of 9111 bp in length
7: gap of unknown length
9: contig of 13152 bp in length
9: gap of unknown length
9: gap of unknown length
0: contig of 16491 bp in length
0: gap of unknown length
1: gap of unknown length
7: contig of 24775 bp in length
2: contig of 24775 bp in length
                                                            length=unknown
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75711. .93797
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59020. .59119
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45768. .45867
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21750. .28521
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13700. .16835
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/45034...177878
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Lau.C., Boffelli,D. and Roe,B.A.
Direct Submission
Submitted (23-NOV-2000) Department Of Chemistry And Biochemistry,
Submitted (73-NOV-2000) Department Of Oval, Room 208, Norman,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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( bases 1 to 179154)
Lau,C., Boffelli,D. and Roe,B.A.
Papio anubis BAC Clone rp41-286p17
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Papio anubis clone rp41-286p17,
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The University Of Oklahoma
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On Feb 15, 2005 this sequence version replaced gi:55701371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lau, C., Boffelli, D. and Roe, B.A. Direct Submission
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3 (bases 1 to 179154)
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1 68161: contig of 68161 bp in length
68162 68261: gap of unknown length
68262 179154: contig of 110893 bp in length.
Location/qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                                     68162.
                                                                       /estimated_length=unknown
                                                                                                                /clone="rp41-286p17"
/clone_lib="RPCI - 41 Male
                                                                                                                                                                             db_xref="taxon:9555"
                                                                                                                                                                                                                                 organism="Papio anubis"
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Papio anubis (olive baboon)
Papio anubis
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On May 5, 2005 this sequence version replaced gi:62702059
One of the University of Oklahoma
Center code:UOKNOR
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Direct Submission
Submitted (23-NOV-2000) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Papio.

1 (bases 1 to 171010)

Lau,C., Boffelli,D. and Roe,B.A.
Papio anubis BAC Clone rp41-339m12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (26-JUL-2005) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Papio anubis clone rp41-339m12, WORKING DRAFT SEQUENCE, 2 ordered
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                                                                         by the finished sequence as soon as it is available the accession number will be preserved.

1 16952: contig of 16952 bp in length 16953 17052: gap of unknown length 17053 171010: contig of 153958 bp in length.

Location/Qualifiers
                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced
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u,C., Boffelli,D. and Roe,B.A.
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,C., Boffelli,D. and Roe,B.A.
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Homo sapiens chromosome 6 clone RP11-189014 map
SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                Submitted (28-MAR-2000) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 194321)
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1 (bases 1 to 194321)

Birren,B., Linton,L., Nusbaum,C.
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* NOTE: This record contains 224 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marguis, N., McCarthy, M., McBwan, P., McKernan, K., McCherters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., McPheeters, R., Meldrim, J., Mornan, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riback, M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Tavers, M., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Smit, A.F.A. & Green, F. (1770-1777)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 24, 2000 this sequence version replaced gi:9799792. All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
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Direct Submission
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Griffin, J.A., Zheng, W., Blake, J.J., Emerling, B.M., Lee, S.Y., Chang, H., Griffin, J.A., Zheng, W., Lee, S., Reddy, R., Khare, R., Forsythe, I.J., Bulloch, S.A., Lee, S., Reddy, R., Khare, R., Chawla, N.K., Baughn, M.R., Burrill, J.D., Ho, A. and Warren, B.A.

LIPID-ASSOCIATED MOLECULES

AL PATENT: JP 2005514007-A 10 19-MAY-2005;

AL INCYTE GENOMICS INC, Bridget A WARREN, Brooke M EMERLING, Ernestine A LEE, Hsin-Ru CHANG, Ian J FORSYTHE, Jennifer A GRIFFIN, Mariah R BAUGHN, Narinder K CHAMLA, Reena HARE, Roopa REDDY, Sally LEE, Sean A BULLOCH, Soo Yeun LEE, Uyen K TRAN, Vicki S ELLIOTT, Tom Y TANG, Umesh BHATIA, John D BURRILL, Julie J BLAKE, Anne HO, Wenjin ZHENG

S Homo sapiens

PN 19-MAY-2005

19-MAY-2005

19-MAY-2005

21-SEP-2001 US 60/34039,02-NOV-2001 US 60/343876, PR

26-OCT-2001 US 60/342166,22-JAN-2002 US 60/340223, PR

18-DEC-2001 US 60/342166,22-JAN-2002 US 60/340223, PR

18-DEC-2001 US 60/342166,22-JAN-2002 US 60/340223, PR

18-DEC-2001 US 60/342166,22-JAN-2002 US 60/371576 PI umesh bhatia,tom y tang, vicki s elliott, uyen k tran, soo yeun PI lee, PI bail, ton y tang, vicki s elliott, uyen k tran, soo yeun PI lee, PI brooke m emerling, ernestine a lee, ian j forsythe, sean a PI brooke m emerling, ernestine a lee, ian j forsythe, sean a PI
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-NOV-1987) McLean J.W., G
Bruno Blvd, So. San Francisco CA 94080
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human mRNA for apolipoprotein(a)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McLean, J.W.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA sequence of human apolipoprotein(a) is homologous to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 13938)
McLean, J.W., Tomlinson, J.E., Kuang, W.J.,
Fless, G.M., Scanu, A.M. and Lawn, R.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apolipoprotein; apolipoprotein A;
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X06290.1 GI:28619
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CSDAEGTAVAPPTVTPVPSLEAPSBOAPTEOREGVOECYHGNGOSYRGTYSTTVTGRT
CQAMSSMTPHSHSRTPEYYPNAGLIMYCRNPDAVAAPYCYTRDBGVUREYCNLTQCS
DAEGTAVAPPTVTPVPSLEAPSBOAPTEORFOVOECYHGNGOSYRGTYSTTVTGRTC
CQAMSSMTPHSHSRTPEYYPNAGLIMYCRNPDAVAAPYCYTRDFGVRWEYCNLTQCSDA
EGTAVAPPTVTPVPSLEAPSBOAPTEORFGVOECYHGNGOSYRGTYSTTVTGRTCQAW
SSMTPHSHSRTPEYYPNAGLIMYCRNPDAVAAPYCYTRDFGVRWEYCNLTQCSDAEGTAVAPPTVTPVPSLEAPSBOAPTEORFGVOECYHGNGOSYRGTYSTTVTGRTCQAWS
SMTPHSHSRTPEYYPNAGLIMYCRNPDAVAAPYCYTRDFGVRWEYCNLTQCSDAEGTA
VAPPTVTPVPSLEAPSBOAPTEORFGVOECYHGNGOSYRGTYSTTVTGRTCQAWSSMT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="liver"
/clone_lib="lambda gt10, lambda ZAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="unnamed protein product; apolipopreprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone_lib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="mkNA"
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89.5%;
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Pred. No. 1.2e-33;
1; Mismatches 17;
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EARSEQAPTEQREOVGECYHONGGSYRGTISTIVICRICQAMSSMTEHSISTIPY PAGLIANYCRINDANAR PYCTRED GFORWEICHTOCGAMSSMTEHSISTERY'S NAGLINNYCRINDANAR PYCTRED GFORWEICHTOCGAMSSMTEHSISTERY'S NAGLINNYCRINDANAR PYCTRED GFORWEICHTOCGAMSSMTEHSISTERY'S NAGLINNYCRINDANAR PYCTRED GFORWEICHTOCGAMSSMTEHSISTERY'S PAGLINNYCRINDANAR PYCTRED GFORWEICHTOCGAMSSMTEHSISTERY'S PAGLINNYCRINDANAR PYCTRED GFORWEICHTOCGAMSSMTEHSISTERY PAGLINNYCRINDANAR PYCTRED GFORWEICHTOCGAMSSMTEHMRRIT BY VANGLINNYCRINDANAR PYCTRED GFORWEICHTOCGAMSSMTEHMRRIT VPSLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAMSSMTPHSHSRTP EYYPNAGLIMMYCRNPDAVAAPYCYTRDPGVRMEYCNLTQCSDAEGTAVAPPTVTPVP SLEAPSEQAPTEQRPGVQECYHGNGQSYRGTYSTTVTGRTCQAMSSMTPHSHSRTPEY GPPSEQDCMFGNGKGYRGKKATTVTGTPCQEWAAQEPHRHSTF1PGTNKWAGLEKNYC RNPDGD1NGPWCYTMNPRKLFDYCD1PLCASSSFDCGKPQVEPKKCPGS1VGGCVAHP ETQGTFGTGLLKEAQLLVIENEVCNHYKYICAEHLARGTDSCQGDSGGPLVCFEKDK) HVQEIEVSRLFLEPTQADIALLKLSRPAVITDKVMPACLPSPDYMVTARTECYITGWG HSWPWQVSLRTRFGKHFCGGTLISPEWVLTAAHCLKKSSRPSSYKVILGAHQEVNLES YPNDGLTMNYCRNPDADTGPWCFTMDPSIRWEYCNLTRCSDTEGTVVAPPTVIQVPSL ILQGVTSWGLGCARPNKPGVYARVSRFVTWIEGMMRNN"

repeat_region repeat_region

7960. .8301

note="direct repeat region

A (22x)"

Sequencing vector: Plasmid; pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.
* NOTE: This is a 'working draft' sequence. It currently

available at:

Additional information on comparative analysis and ordering are

(NHLBI)

Summary Statistics:

(AA 1- 4529)"

/note="direct repeat 3302. .8985

repeat_region

sig_peptide

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SHSRTPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTOCSDAEGTAVAPP
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TPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTP
TPEYYPNAGLIMNYCRNPDAVAAPYCYTRDPGVRWEYCNLTQCSDAEGTAVAPPTVTP
/product="apolipoprotein (a)
436. .7959
                                                 note="signal peptide
                                     .13689
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                                                     to -) "
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AC093405/c
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JOURNAL
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                       http://pga.lbl.gov/cgi-bin/search_cvcgd?type=n&value=Funding agent: Programs for Genomic Applications (NHL)Contact: 'Jody Schwartz' jrschwartz@lbl.gov
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Query Match
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                 Submitted (27-SEP-2002) Genome Sciences, Lawrence Berkeley Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA On Sep 27, 2002 this sequence version replaced gi:15281242. Draft Sequence Produced by Berkeley PGA Web site: http://pga.lbl.gov Center Code: PGABERK Center Project Name: L004-139K21
                                                                                                                                                                                                                                                                                                                                               Martin, J., Hosseini, R., Peng, Y., Peng, Z., Rubin, E.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                   Lemuridae; Lemur.
1 (bases 1 to 150377)
Martin,J., Schwartz,J.R., Hosseini,R., Peng,Y., Peng,Z., Rubin,E.
and Cheng,J.-F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS PHASE2; HTGS DRAFT.
Lemur catta (ring-tailed lemur)
                                                                                                                                                                                                   Martin, J., Schwartz, J.R., Hosseini, R., Peng, Y., Peng, Z.,
                                                                                                                                                                                                                                                                                                                                Cheng, J.
                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC093405 150377 bp DNA
Lemur catta, WORKING DRAFT SEQUENCE, 7
Bac Clone Name: LB2-139K21
                                                                                                                                                             Direct Submission
                                                                                                                                                                                  and Cheng, J.-F
                                                                                                                                                                                                                                                   America
                                                                                                                                                                                                                                                                                     Submitted (23-AUG-2001)
                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lemur catta
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| 13938
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8986. .10011
/note="direct repeat region B (3x)"
13911. .13916
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89.5%;
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Pred. No. 1.2e
1; Mismatches
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                                                                                                                                                  Berkeley National
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KEYWORDS
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VERSION
                                                                                                                                                                    RESULT 13
AX815991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161;
                                       Homo sapiens (human)
                                                                                                                          AX815991
Sequence 64 from Patent
AX815991
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                      AX815991.1 GI:39646630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCCACAC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTTTCCTAGGTCCCGATGGCCTTCAGCATACAGGGTCATCCTGGGCGCACACGAAGAAA 5913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            consists of 7 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                         GAGCAGACATTGCCTTGCTGAAGCTAAGCAGGTACTGGCTCACTTGTGGTTTTTTGCCCCTA 59018
                                                                                                                                                                                                                                                                                                                                                                                                                                            AGAATCTCCAATCAGATGTTCAGCAAATCGAAGTGTCTAGGCTGTTCTTGGAGCCCACCC 59078
                                                                                                                                                                                                                                                                        AGCTGGTGA 59009
                                                                                                                                                                                                                                                                                                                                                                                 AAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTGGTCTTCACCCCA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAAGAAG 72
                                                                                                                                                                                                                                                                                                             CCCTCCTCA 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the accession number will be preserved.

1 10181: contig of 10181 by in length
10182 10281: gap of unknown length
10282 35862: contig of 25581 by in length
35863 35962: gap of unknown length
55428: contig of 19466 by in length
55429 5528: gap of unknown length
55529 64324: contig of 8796 by in length
64325 64424: gap of unknown length
64425 77652: contig of 13228 by in length
77653 77752: gap of unknown length
77653 77752: gap of unknown length
84124: contig of 6372 by in length
84125 8424: gap of unknown length
84125 150377: contig of 6313 by in length
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nilarity 85.2%;
Conservative (
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34125. .84224
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77653. .777
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mol_type="genomic DNA"

db_xref="taxon:9447"
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Pred. No. 1.2e-33;
0; Mismatches 28;
                                                                                                                                                744 bp
WO03066842.
                                                                                                                                                                    DNA
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Best Local S
Matches 147
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TITLE
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Matches 147; Conserv
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   8
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Sequence 3 from Patent W00250290.
AX463624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Susilo,R., Korting,H.C., Gassen,H.G., Hils,M. Method for producing recombinant proteins in m Patent: WO 03066842-A 64 14-AUG-2003; Trommsdorff GmbH & Co.KG Arzneimittel (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                        THROMB X NV (BE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nagai, N., Laroche, Y. and Collen, D.J.
A yeast expression vector and a method
protein by expression in a yeast cell
Patent: WO 0250290-A 3 27-JUN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AX463624.1
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hominidae; Homo.
                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
                                                           CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
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                                   CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA
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                                                                                                     Conservative
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                                                                                                                                                                                 /translation="APSFDCGKPQVEPKKCPGRVVGGCVAHPHSWPWQVSLRTRPGMHFCGGTLISPEWTLTAAHCLEKSPRPSSYKVILGAHQEVNLEPHPGFTEVGETEGETK KDIALLKLSSPAVITDKVIPACLPSBNYVVADRTECFITGMGETGGTFGGLLKEAGL PVIENKVCNRYEFLNGRVQSTELCAGHLAGGTDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSRFVTWIEGVMRNN"
                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="unassigned DNJ
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                     /protein_id="CAD42144.1"
/db_xref="GI:21886385"
                                                                                                                                                                                                                                                                                                     codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                     note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:21886384
                                                                                                                   66.1%;
85.0%;
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                                                                                                  Score 132.6; DB 2
Pred. No. 6.1e-30;
1; Mismatches 25
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Pred. No. 6.1e-30;
1; Mismatches 25;
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LOCUS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
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AX815990
Search completed: May 26, 2006, 15:57:00 Job time: 2038 secs
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                                                                                                                                                                                                                                                                                                                                                                            Bource
                                                             240
                                                                                                                                                                                     300 CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
                                                                                                                                            68 AGAAGTGAACCTCGAATCTCATGTTCAGGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
                                                                                                                                                                                                                                                                                                                                                                            Susilo,R., Korting,H.C., Gassen,H.G., Hils,M. and Pasternack,R. Method for producing recombinant proteins in micro-organisms Patent: WO 03066842-A 63 14-AUG-2003; Trommsdorff GmbH & Co.KG Arzneimittel (DE) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Sequence 63 from Patent WO03066842.
AX815990
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                                                                                                                            AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC
                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Run on:
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                             O
                                                                                                                                                                                                                                               pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
Score
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length: 2000000000
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Gapop 10.0 , Gapext 1.0
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(without alignments)
2505.525 Million cell updates/sec
                                                                                                                                                                                                  Match
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 Minimum Match 0%
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Listing first 45 summaries
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gb_est9: *
gb_gss1: *
gb_gss2: *
gb_gss3: *
gb_gss4: *
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5643
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8622
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                                                                                                                     AI948806
N91337
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) H73861
 BI759134
BG402207
BX453606
DQ048565
CR749293
BX105247
                                                          CB161593
AV661991
AV662084
                                                                                      CB162370
CB161910
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                                      DQ048566 Pan trog1
CR859622 Pongo pyg
H73861 ys12a02.r1
H90220 yu85908.r1
H90220 yu85908.r1
H94305 yq41c07.r1
AI94806 wq26e12.x
N91337 za14105.r1
H60805 yr45g09.r1
CB16370 K-EST0222
CB161910 K-EST0221
CB161593 K-EST0221
CB161593 K-EST0221
CB161593 K-EST0221
AV662084 AV662084
BI759134 603042546
BG402207 602465764
   CR749293 Homo sapi
BX105247 BX105247
                              BX453606 BX453606
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                     DQ048565 Homo sapi
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87.6 87.6	•	87.6	89.2	90.8	91.6	92.4	94.8	97.8	104.4	105.8	105.8	110.2	113.4	115.8	118.2.	120	121.6	123	123	123	123.6	131	131	131.4	
43.7 43.7	43.7	43.7	44.5	45.3	45.7	46.1	47.3	48.8	52.0	52.7	52.7	54.9	56.5	57.7	58.9	59.8	60.6	61.3	61.3	61.3	61.6	65.3	65.3	65.5	
764 864	724	659	765	815	525	782	568	611	707	606	360	768	766	744	589	1042	686	991	984	700	580	526	526	368	
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ALIGNMENTS

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VERSION
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DQ048566
LOCUS
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                                                                                        gene
                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                     2 (bases 1 to 2141)
Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fledel-Alon,A., Tanenbaum,D.M., Civello,D.,
White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
                                                                                                                                                                                                                              Rockville, MD 20850, USA This sequence was made by them based on alignment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nielsen, R., Bustamante, C., Clark, A.G., Glanowski, S., Sackton, T.B., Hubisz, M.J., Fledel-Alon, A., Tanenbaum, D.M., Civello, D., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M. A. Scan for Positively Selected Genes in the Genomes of Humans and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence.
DQ048566
                                                                                                                                                                                                                                                                                     Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pan troglodytes
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                                                                                                                                                                                                                                                                                                                                                                                                                          PLoS Biol. 3 (6), E170 (2005)
                                                                                                         /organism="Pan troglodytes"
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'locus_tag="HC16515"
                                                                                                                                                                                      ocation/Qualifiers
66.9%;
Score 134.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2141 bp
e, VIRTUAL
                                                                                                                                                                                                                                sequencing genomic exons and ordering franslation starts at the beginning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRANSCRIPT, partial sequence,
    80
    14;
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    Length 2141;
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Query Match

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KEYWORDS
SOURCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neuherberg, GERMANY
Clone from S. Wieman, Molecular Genome Analysis, German Cancer Clone from S. Wieman, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project. This clone (DKFZp470G2422) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany. Please contact RZPD for ordering:
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp470G2422 Further information about the clone and the sequencing project is available at http://mips.gsf.de/projects/cdna/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68
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148; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (12-NOV-2004) MIPS, Ingolstaedter Landstr.1, D-85764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The German cDNA Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pongo pygmaeus mRNA; cDNA
CR859622
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/db_xref="Interpro:IPR003016"
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DH10B; sites SfilA + SfilB"
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34. .2466
                                                                                                                                                                                                                                                                                                                                             /note="plasmin (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Pongo pygmaeus"
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/db_xref="taxon:9600"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone="DKFZp470G2422"
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1; Mismatches
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LKKCSGTEGSVVAPPPVVQLNVETPSEEDCMFGNGKYYRCKATTVTGTPCQEWAAQ
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CGKPQVEPKKCPGRVVGGCVANAHSWPWQVSLRTRFGTHFCGGTLISPEWVLTAAHCL
EKSPRPSSYKVILAAHQSVNLEPHYQEIEVGETFADIALKLSSPAVITDKVI
PACLPSPNVVNAGRTECFITGWGETGGTTGAGLLKEAQLPVIENUVCNRYEFLNGRVK
STELCAGHLAGGTDSCQGDSGGPLVCFEKDKYILQGVTSWGLGCARPNKPGVYVRVSR
FVTWIEGVMRNN"

66.9%; Score 134.2; DB 6; Length 2798;

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REFERENCE
AUTHORS
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Email: estewatson.wustl.edu
Insert Size: 1035
High quality sequence stops: 330
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1035
Std Error: 0.00
Seg primer: M13RP1
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                                                                                                                                                                                                                                                                                                                                                        Hominidae; Homo.

1 (bases 1 to 424)

1 (bases 1 to 424)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chiasoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W.,

Chiasoe,S., Dietrich,N., Kucaba,T., Lacy,M., Le,M., Le,N.,

Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N.,

Mardis,E., Moore,B., Morris,M., Parsons,J., Farfer,C., Rifkin,L.,

Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J.,

Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R.

and Marra,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        H73861

ys12a02.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE.214538 5' similar to gb:X05199 PLASMINOGEN PRECURSOR
                                                                                                                                                                              Washington University Scho
4444 Forest Park Parkway,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                    Genome Res. 6 (9),
8889549
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                     Generation and analysis of Genome Res. 6 (9), 807-828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Pred. No. 1.1e-31;
                                                                                                                                                                                                                             School of Medicine way, Box 8501, St. J
                                                                                                                                                                                                                                                                                                                   280,000 human expressed sequence tags (1996)
                                                                                                                                                                                                                                  Louis, MO
                                                                                                                                                                                                                                    63108
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RESULT 4
H90220
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433 bp mRNA linear EST 28-NOV-199: yu85g08.rl Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone IMAGE.240638 5' similar to gb:X05199 PLASMINOGEN PRECURSOR
Email: est@watson.wustl.edu
Insert Size: 1021
High quality sequence stops: 355
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1021 Std Error: 0.00
                                                                                                                                                                                                                                                                    Hominidae; Homo.

1 (bases 1 to 433)

1 (bases 1 to 433)

Hiller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Hiller,L., Clark,N., Kucaba,T., Le,M., Lennon,G., Marra,M.

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and

Wilson,R.
                                                                                                                                                                         Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:214538"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    organism="Homo sapiens"
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85.0%;
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High quality seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R94305
yq41c07.rl Soares fetal liver spleen INFLS Homo sapiens CDNA clone IMAGE.198348 5' similar to gb:X05199 PLASMINOGEN PRECURSOR
                                                                                                                                                                                                                                                          Hominidae; Homo.

1 (bases 1 to 459)

1 (bases 1 to 459)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
           Email: est@watson.wustl.edu
Insert Size: 1004
High quality sequence stops: 293
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                             Washington University School of Medicine
                                                                                                                                                                                   Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMAN);, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC
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Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:9606"
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Pred. No. 2.1e-31;
1; Mismatches 25
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Louis,

MO 63108

Marra, M.,

DB 10; 25;

Indels Length 433;

0

Gaps

0

95

155 127

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REFERENCE
AUTHORS
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                                                                                                                                                                                                                                   TITLE
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                                                                                                                                                                                                 JOURNAL
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cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 535 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   œ
                                                                                                                           Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                        A1948806 466 bp mRNA linear EST 08-MAR-2000 wq26612.x1 NCI CGAP Kidil Homo sapiens cDNA clone IMAGE:2472430 3' similar to gb:\(\overline{X}\)0519\(\overline{9}\) PLASMINOGEN PRECURSOR (HUMAN);, mRNA sequence.
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1 (bases 1 to 466)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              AI948806.1 GI:5741116
                                                                                                                                                                                             Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTCATCTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 293
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db_xref="GDB:3767398"
/db_xref="taxon:9606"
/clone="IMAGE:198348"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66.1%;
85.0%;
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                                                                                                                                                                                                                                     Anatomy Project (CGAP),
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                                                                                                                                             Ph.D.,
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                                                                                                                                                 Michael
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89
                                                                                                                              rax: 314 200 2019
Email: es@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This -------(info@image.llnl.gov) for further information.
                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                       The WashU-Merck EST
Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                               Hominidae; Homo.

1 (bases 1 to 475)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Hillier,L., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Parsons,J., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMAN);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N91337 475 bp mRNA linear EST 03-APR-1996 zal4h05.rl Soares fetal liver spleen INFLS Homo sapiens cDNA clone IMAGE.292569 5' similar to gb:X05199 PLASMINOGEN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 CCTCATCTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                                                                                                                  primer: mob.REGA+ET
                                                                    quality sequence stop: 296
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="NCI GGAP Kid11"
/note="Organ: kidney; Vector: pT7T3D-PacI; Site_1: Not I;
Site_2: Eco RI; Plasmid DNA from the normalized_library
NCI GGAP Kid3 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 132376-1323911,
1456007-1456775, and 1500552-1502855). Subtraction by
Bento Soares and M. Fatima Bonaldo. "
/organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:1444664
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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85.0%;
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                                                                                                                                                                                                                                                             Louis, MO
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REFERENCE
AUTHORS
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VERSION
KEYWORDS
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COMMENT
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                                       gource
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                                                                                           The WashU-Merck EST Project
Unpublished (1995)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Lou
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 339
Source: IMAGE Consortium, LINI
This clone is available royalty-free throug
IMAGE Consortium (info@image.llnl.gov) for
Seq primer: M13RP1
Sequence Stops: 310
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yr45g09.rl Soares fetal liver spleen INFLS Homo sapiens CDNA clone
IMAGE 208288 5' similar to gb:X05199 PLASMINOGEN PRECURSOR
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1 (bases 1 to 481)

1 (bases 1 to 481)

1 (hases 1 to 481)

1 (haller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Hillier, L., Clark, N., Kucaba, T., Le, M., Lennon, G., Marra, M. Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Parcyaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                                                       quality sequence stop: 339.
Location/Qualifiers
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/db_xref="taxon:9606"
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/organism="Homo sapiens"
/mol_type="mRNA"
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85.0%;
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Pred. No. 2.1e-31;
1; Mismatches 25;
                                                                                                                        through LLNL ; contact the v) for further information
                                                                                                                                                                                                                                                              Louis,
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RESULT H60805

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                                                                                                                              source
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                                                                                                                                                                                                       Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        517 bp mRNA linear K-EST0222936 L17N670205n1 Homo sapiens cDNA clone L17N670205n1-42-H08 5', mRNA sequence CB162370
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (human)
                                                                                                                                                          Email: yongsung@mail.kribb.re.kr
Plate: 42 row: H column: 08
High quality sequence stop: 517.
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Unpublished (2002)
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Kim, N.S., Hahn, Y.,
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/db_xref="taxon:9606"
/clone="IMAGE:208288"
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                                                                                                                                            Location/Qualifiers
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85.0%;
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Genome Research Institute of Bioscience & Biotechnology

Korea Research Institute of Bioscience & Biotechnology

Formun-dong Yuseong-gu, Daejeon 305-333, South Korea
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K-EST0221967 L17N670205nl Homo sapiens
L17N670205nl-41-Gll 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                           Email: yongsung@mail.kribb.re.kr
Plate: 41 row: G column: 11
High quality sequence stop: 543.
Location/Qualifiers
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Kim, N.S., Hahn, Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Kim YS
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                                                                                                                     /clone_lib="Li7N670205n1"
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Site_2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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                   66.1%;
Score 132.6; DB 4
Pred. No. 2.2e-31;
1; Mismatches 25
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Pred. No. 2.2e-31;
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Plate: 35 row: F column: 05
High quality sequence stop: 564.
Location/Qualifiers
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Korea Research Institute of Bioscience & Biotechnology
52 Eboeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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CB161593 CB161593
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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                          CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
                                                                                                                                                          CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA
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n,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kin,S., Kim,J.M., Park,H.S., Kim,S.
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/note="Organ: Liver; Vector: pT773D-PacI; Site 1: EcoRI;
/note="Organ: Liver; Vector: pT773D-PacI; Site 1: EcoRI;
/site 2: NotI; The library was contributed by the Soares
laboratory and it was constructed as described by Bonaldo,
M.F., Lennon, G. and Soares, M.B. (1996), Genome Research
6(9): 791-806. RNA was prepared from harvested cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lab_host="Top10F'"
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Pred. No. 2.2e-31;
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
201203, P. R. China
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AV661991 GLC Homo sapiens
AV661991
AV661991.1 GI:9883005
                                                                              AV662084 GLC Homo sapiens
AV662084
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Homo sapiens
Eukaryota; M
                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                               Similarity 85.4
47; Conservative
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                                                                                                                                                                                                                                                                                     AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC
                                                                                                                                                                                                                                                                                                                              ccacrocttggagaagtccccaaggccttcatcctacaaggtcatcctgggtgcacacca
                                                                                                                                                                                                                                                                                                                                                 CCTCATCTTTCTAGGICCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA
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clone is available at CHGC
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                 GI:9883098
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85.0%;
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Pred. No. 2.3e-31;
1; Mismatches 25;
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REFERENCE
AUTHORS
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Insight into hepatocellular carcinogenesis at transcriptome level by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver with carcinoma space. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Zeguang Han Chinese National Human Genome Center at Shanghai Shinese National Homan Genome Center at Shanghai Si Guo Shoujing Road, Zhangjiang Hi-Tech Park, 201203, P. R. China Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
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Hominidae; Homo.
1 (bases 1 to 611)
                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Euarchontoglires; Primates; Cata Hominidae; Homo.

1 (bases 1 to 766)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: hanzg@chgc.sh.cn
This clone is available at CHGC
Location/Qualifiers
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Libzary Preparation: Life Technologies, Inc.
cDNA Libzary Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                              Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                           mRNA sequence.
BI759134
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/dev_stage="Adult"
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Catarrhini;
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                                                                                 Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

E 1 (bases 1 to 859)

National Institutes of Health, Mammalian Gene Collection (MGC)

National Institutes of Health, Mammalian Gene Collection (MGC)

LUppublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: CLONTECH Laboratories, Inc.

CDNA Library Preparation: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium (LLNL)

Lone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           128
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11456 row: l column: 12
High quality sequence stop: 766.
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602465764F1 NIH_MGC_75 Homo sapiens
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/mol_type="mRNA"
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85.0%;
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Search completed: May 26, 2006, 16:10:41 Job time : 4490 secs
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//clone=libannian MGC 15"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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85.0%;
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Pred. No. 2.5e-31;
1; Mismatches 25;
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Maximum Match 100%
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score greater than or equal to the score of the result being printed,
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(without alignments)
3958.819 Million cell updates/sec
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Match
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GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd
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ADQ38544
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ADQ75139
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Acc47280 Human apo
Adc33412 Human apo
Adq75139 Human apo
Adq38545 Human SNP
Aas80436 DNA encod
Ach00783 Human mic
Abn89460 Human mic
Ach00782 Human mic
Ach00782 Human mic
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Adq45152 Myocardia
Aas86437 DNA encod
Aas66111 DNA encod
Adq38544 Human SNP
Aca64741 Apolipopr
Adf43405 Apolipopr
Adf43405 Apolipopr
Aea03076 iNOS nucl
Acc49787 Human lip
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132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6	132.6						132.6		
66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	•	g		σ	
2432	2430	2412	2400	2376	2376	2296	2296	2296	2145	1907	1724	1314	1302	1053	1050	1047	1047	1047	1041	1038	1017	1011	1005	999	786	/83	3
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ALIGNMENTS

RESULT 1
AD045131
ID AD044
XX AD04
XX AD04
XX MYOC
CATC
CATC
XX MYOC
XX MYOC
XX MYOC
XX MYOC
XX MYOC
XX MO20
XX MO20
XX HOME
XX IS-U
PF 22-I
XX 22-I
PF 23--I
PR 30--F
PR 31--F
PR 31--F
PR 31--F
PR 31--F
PR 31--F
PR 31--F
PR 11--F
PR 23--F
PR 11--F
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PR 23--F
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PR 21--F
PR 21--F
PR 21--F
PR 11--F
PR 21--F
PR 21--Myocardial infarction; detection; single nucleotide polymorphism; SNP; cardiant; gene therapy; human; ds. Myocardial infarction-associated SNP flanking transcript, SEQ ADQ45134; ADQ45134 standard; DNA; 201 20-DEC-2002; 2002US-0434778P. 10-MAR-2003; 2003US-0453135P. 30-APR-2003; 2003US-0466412P. 23-SEP-2003; 2003US-0504955P. 18-NOV-2004 (first entry) 22-DEC-2003; 2003WO-US040978 WO2004058052-A2 Homo sapiens Cargill M, 15-JUL-2004. (APPL-) APPLERA CORP. Devlin JJ, Iakoubova ВP ö ID 6797

The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of

Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism the individual's nucleic acids.

in

Claim 7; SEQ ID NO 6797; 145pp; English.

WPI; 2004-533949/51.

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RESULT 2
ADQ45152
ID ADQ4
XX ADQ4
XX Myoc
XX AN
PA 10-
PR 10-
PR 10-
PR 30-
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Best Local S
Matches 155
                                                                                                            20-DEC-2002; 2002US-0434778P.
10-MAR-2003; 2003US-0453135P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-NOV-2004
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90.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13; Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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Sequence

201 BP; 53

A; 54 C; 45 G;

48 T; 0

U; 1 Other;

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The invention relates to a novel method for identifying an individual who can be an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's curcleic acids, where the presence of the SNP is correlated with an callered risk for myocardial infarction in the individual. The invention called the comprises: an isolated nucleic acid molecule comprising at least call molecule comprising at least called expenses given in the specification; an isolated polypeptide contribing an amino acid sequence given in the specification; an antibody chart specification and which is between about 16 and 1000 nucleotides in called polymucleotides in an amplified polymucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in concleic acid molecule; a method of detecting an variant polypeptide; and concleic acid molecule; a method of detecting an variant polypeptide; and a concleic acid molecule; a method of detecting an variant polypeptide; and a concleic acid infarction. The novel detecting method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The converse of the invention may be used in gene therapy. The converse of the semence represents a transcript based contexts sequence.
                                                                polynucleotide sequence represents a transcript-based context sequence which flanks an SNP found in a human myocardial infarction-associated gene of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the individual's nucleic acids.
                                              downloaded from the WIPO website.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Devlin JJ,
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AASB0437
ID AASB
XX AASB
AC AASB
XC AASB
XX DT 13-F
XX DNA
DE DNA
XX DNA
XX DNA
XX Home
XX Home
XX Home
XX Home
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Best Local
               Homo sapiens
                                                   Human;
                                                                           DNA encoding novel human diagnostic protein #16241.
                                                                                                     13-FEB-2002
                                                                                                                                                      AAS80437
                                      food supplement;
                                                                                                                                                                                                                                           129
                                                                                                                                                                                                                                                                                                                                                                      155;
                                                                                                                                                                                                                                                                    69
                                                                                                                                                                                                                                                                                            69
                                        chromosome mapping; gene mapping; gene
upplement; medical imaging; diagnostic;
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
                                                                                                                                                                                                                                                                                  GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
                                                                                                                                                      standard; cDNA; 820
                                                                                                                                                                                                                                                                                                                     CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA
                                                                                                                                                                                                                                                                                                                                   CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA
                                                                                                                                                                                                                                                                    GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                72.0%;
                                                                                                                                                                                                                                                                                                                                                                      <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                      Score 144.4; DB 1
Pred. No. 5.1e-40;
0; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                        17;
                                        genetic of
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                                                                                                                                                                                                                                                                                                                                                                                                 201;
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RESULT 4
AAS66111
AAS6 AS6
XX
AC AAS6
XX
AC AAS6
XX
DT 13-F
XX
DE DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cc sequences. (I) is useful as hybridisation probes, polymerase chain cc reaction (PCR) primers, oligomers, and for chromosome and gene mapping, cl in diagnostics as expressed sequence tags for identifying expressed cc in diagnostics as expressed sequence tags for identifying expressed cc genes. (I) is useful in gene therapy techniques to restore normal cc activity of (II) or to treat disease states involving (II). (II) is cuseful for generating antibodies against it, detecting or quantitating a cc useful for generating antibodies against it, detecting or quantitating a cc polypeptide in tissue, as molecular weight markers and as a food cc supplement. (II) and its binding partners are useful in medical imaging cc fistes expressing (II). (I) and (II) are useful for treating disorders involving abservant protein expression or biological activity. The cc diagnostics, forensics, gene mapping, identification of mutations in compositive for genetic disorders or other traits to assess biodiversity amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at
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                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 16241; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAR-2001; 2001WO-US008631
 DNA encoding
                                  13-FEB-2002
                                                                     AAS66111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200175067-A2
                                                                                                   AAS66111 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-639362/73
                                                                                                                                                                                                                           129
                                                                                                                                                                                                                                                              176
                                                                                                                                                                                         236
                                                                                                                                                                                                                                                                                                                               116 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA
                                                                                                                                                                                                                                                                                              69
                                                                                                                                                                                                                                                                                                                                                                                                    154;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         820
                                                                                                                                                                                                             ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
                                                                                                                                                                                                                                                                              GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC 128
                                                                                                                                                                                                                                                                                                                                                     CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA
                                                                                                                                                                                                                                                            GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC
                                                                                                                                                                                         ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP;
                                  (first entry)
 novel human diagnostic protein #1915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 A; 203 C; 209 G; 199 T; 0 U; 0 Other;
                                                                                                     CDNA; 820
                                                                                                                                                                                                                                                                                                                                                                                                                     72.0%;
89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 144.4; DB 5
Pred. No. 9.7e-40;
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                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to isolated polynucleotide (I) and polypeptide (II) cequences. (I) is useful as hybridisation probes, polymerase chain CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed CC in diagnostics as expressed sequence tags for identifying expressed CC genes. (I) is useful in gene therapy techniques to restore normal CC cuseful for generating antibodies against it, detecting or quantitating a CC useful for generating antibodies against it, detecting or quantitating a CC polypeptide in tissue, as molecular weight markers and as a food CC gupplement. (II) and its binding partners are useful in medical imaging CC involving aberrant protein expression or biological activity. The CC diagnostics forensics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in CC electronic format directly from MIPO at CC from with a control of the control of contr
                                                                                                                                                                                                                                                                      Matches 154;
                                                                                                                                                                                                                                                                                            Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                         Sequence 820 BP; 209 A; 203 C; 209 G; 199 T; 0 U; 0 Other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1915; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; ABG01924.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001-639362/73.
                                                                                       176
236
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                                                                                     GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC
                                                                                                                                                                            CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 175
                            ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
                                                                                                                                                                                                                       CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA
ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Liu C,
                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-00649167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-00540217
                                                                                                                                                                                                                                                                                            72.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŢΥ
                                                                                                                                                                                                                                                                      Score 144.4;
Pred. No. 9.7e
1; Mismatches
                                                                                                                                                                                                                                                                                                9.7e-40;
                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                                   Length 820;
                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                           128
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RESULT 5 ADQ38544 ID ADQ3

ADQ38544 standard; DNA; 3756 BP.

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18-NOV-2004 (first entry)

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ce has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleic acids, where the presence of the SNP is correlated with an callered risk for myocardial infarction in the individual's conclude acids, where the presence of the SNP is correlated with an callered risk for myocardial infarction in the individual. The invention callered risk for myocardial infarction in the individual. The invention callered risk for myocardial infarction in the individual. The invention callered comprising at least a contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino called sequence given in the specification; an antibody that specifically binds to the polymeptide or its antigen-binding callered polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in calleritying an agent useful in callerity comprising the callerity a kit for detecting an SNP in a nucleic acid, comprising the callerity and a method of detecting an SNP in a nucleic acid, comprising the callerity and a method of detecting an snP in a nucleic acid molecule; and an enzyme; a method has cardiant activity. The nucleic acids of the invention may be useful in treating or preventing an composition for treating or preventing myocardial infarction. This composition for treating or preventing myocardial infarction. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.
20-DEC-2002;
10-MAR-2003;
30-APR-2003;
23-SEP-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; SEQ ID NO 207; 145pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism the individual's nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Myocardial infarction; detection; single nucleotide polymorphism; SNP cardiant; gene therapy; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-533949/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiant; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human SNP containing myocardial infarction-associated gene, SEQ ID 207
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (APPL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-2003; 2003WO-US040978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention relates to a novel method for identifying an individual who
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLERA CORP.
  3756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Devlin JJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002US-0434778P.
2003US-0453135P.
2003US-0466412P.
2003US-0504955P.
  BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy; human; gene;
  1017
A; 965 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Iakoubova
  914 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
  839 T; 0 U;
  21 Other;
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CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68

3027

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Query Match Best Local S Matches 155

Similarity

72.0%; 90.1%;

Score 144.4; I Pred. No. 1.9e 0; Mismatches

.9e-39 DB 13; 17;

Indels Length

Gaps

3756 0

Conservative

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RESULT 6
ACA64741
ID ACA6
XX ACA64741
ACA6
XX ACA64741
ACA6
XX ACA64741
ACA6
XX ACA64741
ACA6
ACA64741
                    The invention relates to a mammalian cell receptor, useful in the creatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs). CR Also included are a mammalian cell useful in the treatment of cancer creations included are a mammalian cell useful in the treatment of cancer creations (M1) a tumouricidal immunocyte population in vivo in a mammalian cell useful in the treatment of cancer creceptors for immunosuppressive fatty acids, ceramides, glycosphingolipids and induces creceptors for immunosuppressive fatty acids, ceramides, glycolipids, comparation of cancer comprising a sialylated glycans, lipopeptides and proteoglycolipids gangliosides, comparantigen (SAg) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer of cancer comprising a construct useful in the treatment of a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which compared into a proteoglycolipids are inactivated or concer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumour associated lipids to contact immunocytes, in which creceptors for the lipids are inactivated or deleted to produce a cumouricidal immunocyte population, and administering the tumouricidal APC contact APCs, in which receptors for the host), producing (M3) a tumouricidal APC contact APCs, in which receptors for the treatment of contact apcs at the conjugated to a superanticidal APC contact APCs, in which receptors for the host), producing a tumour associated lipids to contact application are represented applied are confidented in a mammal (by allowing a tumour associated lipids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.
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    population ex vivo in a mammal (by allowing a tumour contact APCs, in which receptors for the tumour case inactivated or deleted to produce a tumouricidally
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry
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oxide synthase; gene; ds.
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Pred. No. 3.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2503 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC introduced, (2) treating a tumor or neoplastic disease in a subject; (3) Cc cells useful to treat a tumor or neoplastic disease in a subject; (4) an CC apoptotic cell preparation or lysate useful for treating a tumor or neoplastic disease in a subject; (4) an CC apoptotic cell preparation or lysate useful for treating a tumor or CC neoplastic disease in a subject, comprising a cell population that has been transfected with naked DNA encoding a superantigen, and treated to cundergo apoptosis or lysis; and (5) a cell that has ingested or been transfected with the above apoptotic preparation or lysate, thus, creating the cell effective in presenting material expressed from CC transfecting nucleic acid or material ingested to the immune system of a mammal to elicit an anti-tumor immune response. The composition and CC methods are useful for treating tumors or neoplastic diseases. The present sequence represents an iNOS nucleotide sequence, which is used in present is not represented in the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 154; Conserv
                                                                                                                                                                                                                      Human; lipid-associated molecule; LIPAM; cytostatic; cerebroprotective; antiarteriosclerotic; anti-HIV; antiallergic; anti-HIV; antiallergic; anti-HIV; anticonvulsant; noutropic; anti-HIV; antibacterial; virucide; protozoacide; antiparasitic; antilipaemic; AIDS; gene therapy; cell proliferative disease; cancer; atherosclerosis; ulcer; surcimmune disease; inflammatory disease; allergy, neurològical disorder; stroke; Parkinson's disease; epilepsy; gastrointestinal disorder; cirrhosis; cardiovascular disorder; myocardal infarction; obesity; metabolic disorder; developmental disorder; endocrine disorder; stroke; infection; lipid metabolism disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                exogenous nucleic acid encoding a superantigen expressed in the cell which cell also produces or expresses all alpha-anomers of monoglycosylceramide or diglycosylceramide, where expression of the superantigen and the mono- or diglycosylceramide is capable of elician anantitumor immune response in a mammal into which the cell is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The inve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10422 BP; 3020 A; 2386 C;
                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lipid-associated molecule LIPAM-10 encoding cDNA SEQ ID NO:27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACC49787 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to a composition for treating a tumor or neoplastic ease in a subject. Also described: (1) a mammalian cell comprising an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9634 CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG 9805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                           Location/Qualifiers
                                                                   /product= "LIPAM-10"
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89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2503 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2513 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the cell,
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Best Local Sim:
Matches 154;
                                                                                                                                                                                                                                                                                                                                           antiplear, the artivities, antibacterial, virucide, protozoacide, cardiant, cantiparasitic and antilipaemic activities, and can be used in gene therapy. The LIPAM polypeptides and polymucleotides are useful in the diagnosing, treating and preventing diseases or conditions associated with decreased expression or overexpression of LIPAM, such as cell proliferative diseases (e.g. cancer or atherosclerosis), autoimmune/ inflammatory diseases (e.g. AIDS or allergies), neurological disorders (e.g. stroke, Parkinson's disease or epilepsy), gastrointestinal (e.g. ulcer or cirrhosis), cardiovascular (e.g. myocardial infarction), culcer or cirrhosis), cardiovascular (e.g. myocardial infarction), cardiovascular (e.g. myocardial infarction), condisorders infections (e.g. bacterial, viral, parasitic or pulmonary disorders, infections (e.g. bacterial, viral, parasitic or protozoal), candiovascular (e.g. bacterial, viral, parasitic or protozoal), candioscapences of lipid metabolism. They are also useful in assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of LIPAM. They lipids or their fragments are useful in screening compounds for effectiveness as agonist or antagonist of the polypeptides, or in altering the expression of the target polynucleotide and compounds that specifically bind to or modulate the activity of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-SEP-2001; 2001US-0324039P.
26-CCT-2001; 2001US-03448197P.
02-NOV-2001; 2001US-0343876P.
30-NOV-2001; 2001US-0334211P.
14-DEC-2001; 2001US-034223P.
18-DEC-2001; 2001US-0342166P.
22-JAN-2002; 2002US-0377576P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Warren BA
Baughn MR
Tran UK,
Zheng W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC49778 to ACC49794 encode the human lipid-associated molecule proteins given in ABR43296 to ABR43312, designated LIPAM-1 to LIPAM-17 (I). (I) have cytostatic, antiarteriosclerotic, anti-HIV, antialleggic, nootropic, cerebroprotective, antiparkinsonian, anticonvulsant, antiinflammatory,
                                                                                                                                                                                                                                                                                           Sequence 13869 BP; 3589 A; 3879 C; 3551 G; 2850 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New human lipid-associated molecules (LIPAM) useful for diagnosing, treating and preventing diseases or conditions associated with aberrant LIPAM expression, e.g. cancer, AIDS, atherosclerosis or infections.
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                                                                                                                                                                                                                                                                                                                              polypeptide
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                                                                       13210
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                                                                                                                                                                                                                                      Similarity
                                                                                                GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC
                                                                                                                                                                  CTCATCTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACAACCAA
                                                                       GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC
                                                                                                                                               CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA
 ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG
                                ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
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Chawla NK,
Elliott VS,
                                                                                                                                                                                                                     Conservative
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, Khare R,
Tang YT,
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                                                                                                                                                                                                                                    Score 144.4;
Pred. No. 3.
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                                                                                                                                                                                                                         Mismatches
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Bhatia U,
                                                                                                                                                                                                                       3.5e-39;
ies 17;
                                                                                                                                                                                                                                                          DB 10;
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Lee S, Bulloch
Burrill JD, Bla
                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                          Length 13869;
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loch SA, Lee S!
Blake JJ, Ho
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   13321
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RESULT 11
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Best Local Simi
Matches 154;
                                                                                                                                                                                                                                                                                                 The invention relates to a new compound, 8-50 nucleobases in length targeted to a nucleic acid molecule encoding human apolipoprotein(a), specifically hybridizes with and inhibits the expression of human apolipoprotein(a). The antisense compounds are useful for preparing a composition for treating abnormal lipid or cholesterol metabolism, atherosclerosis or cardiovascular disease. The present sequence represents a DNA encoding the human apoliprotein(a) (GenBank accession No.NM_005577)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                   New antisense compound, useful for preparing a composition for abnormal lipid or cholesterol metabolism, atherosclerosis or cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-AUG-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Apolipoprotein(a); antiarteriosclerotic; cardiant; gene therapy; human;
gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-AUG-2003
           AD033412;
                               ADO33412 standard; DNA; 13938 BP
                                                                                                                                                                                                                                                                               Sequence 13938 BP; 3613 A; 3889 C; 3560 G;
                                                                                                                                                                                                                                                                                                                                                                                                              Example 13; Page 92-112; 120pp; English
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                                                                                                                                        GAAGTGAACCTCGAATCTCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCCC
                                                                                                                                                     GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC
                                                                                                                                                                                     CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA
                                                                                                                                                                                                         CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA
                                                                                          ACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGCCTGCCGTCATCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graham MJ
                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                             72.0%;
89.5%;
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                                                                                                                                                                                                                                               Score 144.4;
Pred. No. 3.5
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                               .5e-39;
                                                                                                                                                                                                                                                            BG
                                                                                                                                                                                                                                                                                  2876 T; 0
                                                                                                                                                                                                                                     17;
                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                          Length 13938;
                                                                                                                                                                                                                                                                                  u; o
                                                                                                                                                                                                                                                                                   Other;
                                                                                                                                                                                                                                      0,
                                                                                             13321
                                                                                                                   180
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                68
                                                                                                                                                                                         13209
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                                                                                                                                                                                                                                            CC cholesterol levels, lipid levels, triglyceride levels, control cardiovascular disportants and mostropic activities and may contest and notropic activities and may continue in vivo in order to address a condition associated with abnormal control or cholesterol metabolism. The compound may be useful for cholesterol levels, lipid levels, fatty acid levels, acute phase condition associated with abnormal control of the same chylomicrons and thus may be utilised during treatment of contesterol levels, lipid levels, fatty acid levels, acute phase contested and chylomicrons and thus may be utilised during treatment of contested and chylomicrons and thus may be utilised during treatment of contested and chylomicrons and thus may be utilised during treatment of contested and chylomicrons and thus may be utilised during treatment of contested and the same in the contested during treatment of contested and the children, hypertholesterolaemia, contested and the children, hyperthyroidism, hypertension, contested nervosa, Werner's syndrome, hepatoma, multiple myeloma, uracemia, contested nervosa, werner's syndrome, hepatoma, multiple myeloma, uracemia, contested nervosa, werner's syndrome, hepatoma multiple myeloma, uracemia, contested nervosa, hepatoma multiple myeloma, uracemia, contested nervosa, werner's syndrome, hepatoma multiple myeloma, uracemia, contested nervosa, werner's syndrome, hepatoma multiple myeloma, uracemia, contes
                                                                                               Matches
                                                                                                                      Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apolipoprotein B; ApoB; cardiovascular; antiarteriosclerotic; antilipaemic; antidiabetic; anorectic; cardiant; vasotropic; anabolic; eating disorder; cytostatic; endocrine; vasotropic; neuroprotective; nootropic; lipid; cholesterol metabolism; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; von Gierke's disease; lipodystrophy; Cushing's syndrome; von Gierke's disease; lipodystrophy; Cushing's syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel antisense compound where the compound hybridises to and inhibits expression of mRNA encoding human apolipoprotein B (ApoB) after 16-24 hours by at least 30% in 80% confluent HepG2 cells in culture at a concentration of 150 nM. The compound of the invention demonstrates cardiovascular, antiarteriosclerotic, antilipaemic, antidabetic, anorectic, cardiant, avasotropic, hypotensive, anabolic, eating disorder-related, cytostatic, vasotropic, hypotensive, anabolic, eating disorder-related, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antisense oligonucleotide compound that inhibits expression of mRNA encoding human apolipoprotein B, useful for treating hyperlipidemia, diabetes, obesity, von Gierke's disease, lipodystrophies, Cushing's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sexual ateliotic dwarfism; hyperthyroidism; hypertension; anorexia nervosa; Werner's syndrome; hepatoma; multiple myeloma; uraem: impotence; obstructive liver disease; Alzheimer's; dementia; diabetes; obesity; atherosclerosis; human; ds; apolipoprotein(a); Lp(a).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-NOV-2002; 2002US-0426234P
15-MAY-2003; 2003WO-US015493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-AUG-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crooke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-2003; 2003WO-US036411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAY-2004.
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                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 57; SEQ ID NO 860; 483pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ISIS-) ISIS PHARM INC
                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   apolipoprotein(a)
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                                                                                                                                                                                                     13938 BP; 3614 A; 3889 C; 3560 G;
                   CTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCAA 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Graham M,
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                      72.0%;
89.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [Lp(a)] DNA - SEQ
                                                                                                  ۲.
                                                                                               Score 144.4; DB 1
Pred. No. 3.5e-39;
1; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         960
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                                                                                                                                                        DB 12;
                                                                                                                                                                                                                2875 T;
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CATCCTGGGTGCACACCAA 13209
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                                                                                                           Gaps
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13150

CACTGCTTGAAGAAGTCCTCAAGGCCTTCATCCTACAAGGT

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GAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCCC

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ARESULT 12
AD075139
XX AD075
XX AD076
X
                                                                 CC length targeted to a nucleic acid molecule encoding apolipoprotein(a), where the compound is at least 70% complementary to the nucleic acid complementary to the expression of apolipoprotein(a) manA by at least 10%. Also described are: a method of complementary and aliesase or condition associated could be apolipoprotein(a); a diagnostic method for identifying a disease state, comprising identifying the presence of apolipoprotein(a) in a sample comprising to a modulator of comprising the presence of apolipoprotein(a) in a sample consist on a sary device comprising (1); and a method of inhibiting the compression of apolipoprotein(a), comprising contacting a biological compound, where the synthetic antisense compound comprises 13-30 compound, where the synthetic antisense compound comprises 15-30 compound comprises and compositions of the present invention are useful for the constitution are useful for the constitution are useful for the constitution and the compound compound comprises and compositions of the present invention are useful for the constitution and compositions are useful for the consecution of activity of apolipoprotein(a), coronary artery disease and/or their combinations. This sequence encodes thuman apolipoprotein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New antisense oligonucleotide compounds, useful for diagnosing, preventing and/or treating conditions with aberrant expression of apolipoprotein(a), such as atherosclerosis, hypercholesterolemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-AUG-2001;
02-JUN-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crooke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-OCT-2003; 2003US-00684440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 13; SEQ ID NO 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coronary artery disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ISIS-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention describes a new
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DB; ADQ75209.
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2003US-0475402P
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Sequence 13938 BP; 3613 A;

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3560 G;

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RESULT 13
ADQ38545
ID ADQ38
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XX Myoca
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Best Local (
B contiguous nucleotides where one of the nucleotides is an SNP given the specification or its complement and encoding any one of the and acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an ar that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP polynucleotide, a buffer and an enzyme; a method of detecting an SNP polynucleotide.
                                                                                                                                                                                                                                                                     The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least further comprises: an isolated nucleic acid molecule comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorph the individual's nucleic acids.
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10-MAR-2003; 2003US-045313P.
30-APR-2003; 2003US-0466412P.
23-SEP-2003; 2003US-0504955P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cargill M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cardiant; gene therapy; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myocardial infarction; detection; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human SNP containing myocardial infarction-associated gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-NOV-2004 (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (APPL-) APPLERA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13270
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Pred. No. 3.5e-39;
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Best Local :
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used
                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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                                                                                                 Claim 1; SEQ ID NO 16240; 103pp; English
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23-AUG-2000;
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Pred. No. 3.5e-39;
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                                                                                                                                                                        06-FEB-2002;
21-FEB-2002;
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Recombinant production of plasminogen signal peptide that can be removed by antithrombotic and anticoagulant.

as a fusion protein comprising proteolysis is useful as an

WPI; 2003-697451/66

5 ₽ S र् Search completed: May 26, 2006, 14:14:02 Job time : 357 secs 밁 The present invention relates to a method of producing a recombinant CC functional plasminogen in microorganisms. The method comprises a sequence cc encoding at least a functional part of such a plasminogen and a sequence cc encoding a signal peptide that are fused together, where the two sequences are linked through codons that encode a protease cleavage site cc to allow removal of the signal peptide. The plasminogen is used to screen cc for plasminogen activators. Both plasminogen and plasmin, prepared from cc treatment/prevention, are used for treatment of wounds and the creating a wide variety of conditions, e.g. cardiac infarct, stroke, cc trombosis, restenosis, hypoxia, ischaemia, vascular inflammation, cc plumonary embolism, conjunctivitis (plasminogen type-I deficiency), burns cc and disseminated intravascular coagulation. The present sequence is a cc coding sequence used in the exemplification of the invention Query Match 66.1%; Score 132.6; DB 10; Length 744; Best Local Similarity 85.0%; Pred. No. 1.3e-35; Matches 147; Conservative 1; Mismatches 25; Indels 0; Sequence 744 BP; 177 A; 169 C; 207 G; 191 T; 0 U; 0 Other; Claim 25; Page 68-69; 140pp; German. 234 AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC 293 83 CACACGAAAAGATATTGCCTTGCTAAAGCTAAAGCAGTCCTGCCGTCATCACTG 346 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127 0, Gaps 0

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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM nucleic - nucleic search, using sw model
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                 Score
                 seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Issued Patents_NA:*

1: /BMC Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*

2: /EMC_Celerra_SIDS3/ptodata/2/ina/6\(\bar{A}\)_COMB.seq:*

3: /EMC_Celerra_SIDS3/ptodata/2/ina/6\(\bar{A}\)_COMB.seq:*

4: /EMC_Celerra_SIDS3/ptodata/2/ina/6\(\bar{A}\)_COMB.seq:*

5: /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*

6: /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*

7: /EMC_Celerra_SIDS3/ptodata/2/ina/P_COMB.seq:*

9: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*

10: /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
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Match Length DB
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200.6
1 ttgacatcctcatctttct.....tcttcaccccacgctggtga 201
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   GenCore version 5.1.8 Copyright (c) 1993 - 2006 Biocceleration Ltd
   US-09-949-016-146441
US-09-949-016-15854
10 5200340-5
US-10-000-489-53
US-10-000-986A-53
US-10-000-986A-53
US-07-750-080A-18
US-08-651-472-18
US-08-651-472-18
US-08-651-2012-4
2 US-08-643-219-12
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2 US-08-832-0878-12
2 US-08-831-350-12
2 US-08-924-287A-12
3 US-08-924-287A-12
3 US-08-93-13-154-12
3 US-08-93-42-87A-12
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3 US-08-93-42-87A-12
3 US-08-93-42-87A-12
3 US-08-93-42-87A-12
3 US-08-93-93-16-4112
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3 US-08-93-94-016-4112
3 US-08-839-078-1
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Sequence 53, Appl
Sequence 53, Appl
Sequence 53, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 12, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 17, Appl
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Sequence 15854, A
Patent No. 5200340
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	US-09-949-016-15425	US-09-949-016-130515	US-09-949-016-130514	US-09-621-976-141	US-09-513-999C-16218	US-09-949-016-13407	US-10-652-164-3	US-09-811-825A-3	US-09-949-016-14837	US-09-949-016-14150	US-09-949-016-14948	US-08-892-544-1	US-08-266-407A-1	US-08-456-840-1	US-08-892-544-21	US-08-892-544-19	US-08-266-407A-21	US-08-266-407A-19	US-08-456-840-21	US-08-456-840-19	US-08-892-544-13	US-08-266-407A-13
÷	Sequence 15425, A			Sequence 141, App		13407,	Sequence 3, Appli				14948,		۲	Sequence I, Appli	21,		•	19	117	,		13,

ALIGNMENTS

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THER

TILLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 146441

LENGTH: 601
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; ORGANISM: Human
US-09-949-016-146441
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                    181
                                                                                                                121
                                                                                                                                                       356
                                                                                                                                                                                                                                    296 TTGACRTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATC
                                                                                                                                                                                                                                                                                                                191; Conservative
                                                                                                                                                             61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAA/FRO
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                                                                                                  TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAG
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                                                                                                                                                       CACACCAAGAAGTGAATCTCGAACCGCATGTTCAGGAA
                                  GTCTTCACCCCACGCTGGTGA 201
TGGAGCCCACACGAAAAGATATTGCCTTTGCTAAAGCTAAGCAGGTACTCGTTCACCTGTG
                                                                                                                                                                                                                                                                                                                                  93.4%;
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Pred. No. 4.9e-55;
2; Mismatches 8
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Sequence 15814, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: MITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 5000-09-08

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US-09-949-016-15854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,Patent No. 5200340

APPLICANT: FOSTER, DONALD C.;MULVIHILL, EILEEN R.;O'HARA,
PATRICK J.;PINGEL, KURT;YOSHITAKE, SHINJI
TITLE OF INVENTION: THROMBIN-ACTIVATED TISSUE PLASMINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-949-016-15854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTIVATORS
                                                                                                                                                                                                                                                                    Query Match 66.1%; Score 132.6; DB 1
Best Local Similarity 85.0%; Pred. No. 8.9e-36;
Matches 147; Conservative 1; Mismatches 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 34
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 22-MAY-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1724
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                                                                                                                                     CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA
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       AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC
                                          AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCCTGTTCTTGGAGCC
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95.0%;
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US-09-992-0958-53
Sequence 53, Application US/09992095B; Patent NO. 6989262; GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR PPLICATION NUMBER: PCT/IB01/01715
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR APPLICATION NUMBER: US 60/305,456
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/302,277
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR FILING DATE: 2001-06-15
PRIOR FILING DATE: 2001-06-15
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US-10-000-489-53
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Best Local Similarity
Matches 147; Conserv
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SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Benjanin, Stephane
APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS
FILE REFERENCE: 91.US6.DIV
CURRENT APPLICATION UNMERR: US/10/000,489
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 53, Ap
Patent No. 6794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: polyA_signal
LOCATION: 1869..1874
NAME/KEY: polyA_site
LOCATION: 1892..1907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1907
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 1044..1664
NAME/KEY: 3'UTR
LOCATION: 1665..1907
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LOCATION: 1..10
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Pred. No. 9.3e-36;
1; Mismatches 25
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APPLICANT: Benjanin, Stephane APPLICANT: Tanaka, Hiroaki TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND FILE REFERENCE: 91.US5.DIV

USES

CURRENT APPLICATION NUMBER: US/09/992,095B

RIOR APPLICATION NUMBER: US 09/924,340

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PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR ELING DATE: 2001-08-06
PRIOR PPLICATION NUMBER: US 60/305,456
PRIOR PPLICATION NUMBER: US 60/302,277
PRIOR PPLICATION NUMBER: US 60/302,277
PRIOR PILING DATE: 2001-06-29
PRIOR PRIOR DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/298,698
PRIOR PILING DATE: 2001-06-15
PRIOR PPLICATION NUMBER: US 60/293,574
PRIOR PILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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LENGTH: 1907
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Best Local
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SOFTWARE: JPatent
                                                                         CURRENT APPLICATION NUMBER: US/10/000,986A
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US 09/924,340
PRIOR FILING DATE: 2001-08-06
PRIOR APPLICATION NUMBER: PCT/IB01/01715
PRIOR FILING DATE: 2001-08-06
                                                                                                                                                                                                             APPLICANT: Tanaka, Hiroaki
TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
FILE REFERENCE: G-091US09DIV
                                                                                                                                                                                                                                                      APPLICANT: Benjanin,
APPLICANT: Tanaka, F
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LOCATION: 1..1043
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LOCATION: 1892..1907
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                                    APPLICATION NUMBER: US 60/305,456 FILING DATE: 2001-07-13
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                    APPLICATION NUMBER: US 60/302,277
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2001-06-29
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85.0%;
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SOFTWARE: JPatent
SEQ ID NO 53
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Best Local S
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                                                                                                                                                 ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION NUMBER: US/07/750,080A
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LOCATION: 1044..1664
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LOCATION: 1..1043
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LOCATION: 1665..1907
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APPLICANT: SCHEIFLINGER,
APPLICANT: FALKNER, F. G
CLASSIFICATION:
ATTORNEY/AGENT INFO
NAME: BENT, Step
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                FILING DATE: 19910826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
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147; Conserv
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1800 Diagonal Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                             INFORMATION:
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85.0%;
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Pred. No. 9.3e-36;
                                                                                                                                                                                                                                                     Version
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US-08-651-472-18
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US-07-750-080A-18
            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,472
FILING DATE:
CLASSIFICATION OBTA:
CLASSIFICATION DATA:
APPLICATION OBTA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18, Application US/08651472 Patent No. 6103244
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INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                              ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FALKNER, Falko Gunter
APPLICANT: PFLEIDERR, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFCIENCY VIRUS TYPE 1
TITLE OF INVENTION: (HIV-1) ANTIGENS
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REFERENCE/DOCKET NUMBER: 30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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147; Conservative
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?R: 30472/106 IMMU
30472/166/IMMU
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US-08-651-472-18
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/358;928
FILING DATE:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION NUMBER: US 07/750,080
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DORNER, Friedrich
APPLICANT: SCHEIFLINGER, Friedrich
APPLICANT: FALKNER, Falko Gunter
APPLICANT: FALKNER, Michael
TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC
TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFCIENCY VIRUS
TITLE OF INVENTION: (HIV-1) ANTIGENS
NUMBER OF SEQUENCES: 95
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
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INFORMATION FOR SEQ ID NO:
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DESCRIPTION:
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LENGTH: 2296 base pair
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TYPE: nucleic acid
STRANDEDNESS: single
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Synthetic DNA oligonucleotide
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85.0%;
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                            30472/166/IMMU
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Pred. No. 1e-35;
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2296 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: 1inear
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US-09-192-012-4
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CLONE: pN2gpt-LPg
US-08-358-928-18
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CONTROL HOMO SapienS
FEATURE:
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(2430)
OTHER INFORMATION: human plasminogen
US-09-192-012-4
                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Inhibition of Angiogenesis by Delivery (
TITLE OF INVENTION: Encoding Anti-Angiogenis Polypeptides FILE REPERENCE: 0.18484-000110US 
CURRENT APPLICATION NUMBER: US/09/192,012A 
CURRENT FILING DATE: 1998-11-13 
EARLIER APPLICATION NUMBER: US 60/066,020 
EARLIER APPLICATION NUMBER: US 60/066,020 
EARLIER FILING DATE: 1997-11-14 
NUMBER OF SEQ ID NOS: 9 
SOFTWARE: Patentin Ver. 2.0 
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09192012A Patent No. 6475784
GENERAL INFORMATION:
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Matches
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                                                                                                                                                                                                                        Query Match
Best Local Similarity
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APPLICANT: Megabios Corporation
APPLICANT: Pfizer, Inc.
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DESCRIPTION: Synthetic DNA oligonucleotide
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TELEFAX: (
TELEX: 904
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147; Conserv
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CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
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                                                                                                                                                                CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 67
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                                                                                        AGAAGTGAACCTCGAATCTCATGTTCAGGAAATTGAAGTGTCTAGGCTGTTCTTGGAGCC
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(202)672-5399
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85.0%;
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85.0%;

    Mismatches

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                                                                                                                                                                                                                          Score 132.6; DB 3;
Pred. No. 1e-35;
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RESULT 11
US-08-643-219-12
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RESULT 12
US-09-131-995-12
; Sequence 12, Application US/09131995
; Patent No. 5972896
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: ISM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 2497 base pairs
TYPE: nucleic acid
STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 59
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
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100 Abbott Park Road
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NOVEL ANTIANGIOGENIC PEPTIDES
AND METHODS FOR INHIBITING AN
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GENERAL INFORMATION:
APPLICANT: Davidson,
TITLE OF INVENTION:
TITLE OF INVENTION:

, Donald J.
NOVEL ANTIANGIOGENIC PEPTIDES
AND METHODS FOR INHIBITING ANGIOGENESIS

127 2031

67

NUMBER OF SEQUENCES: 14
CORRESSONDENCE ADDRESSES: Abbout Laboratories
STREET: 100 Abbout Park Road

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RESULT 13
US-08-832-087B-12
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2497 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/832,08
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Casuto, Dianne 40,943 REGISTRATION NUMBER: 59. REFERENCE/DOCKET NUMBER: 59. TELECOMMUNICATION INFORMATION: 847-938-3137
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MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
ZIP: 60064
COMPUTER READABLE FORM:
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                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                         APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 100 Abbott
CITY: Abbott Park
STATE: IL
COUNTRY: USA
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                           COUNTRY:
                                                     STATE:
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                                                                                     STREET:
                                                                                                       ADDRESSEE:
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al Similarity 85.0%;
147; Conservative
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                                                                    Abbott
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bbott Park
                                     USA
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                                                                                                                                                                                              Donald J.
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Pred. No. 1e-35;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES,
TITLE OF INVENTION: POLYNUCLECTIDES ENCODING SAME AND METHODS
TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2497 base pair
              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VEFEION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,3
PILING DATE: 05-MAY-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2
CURENT APPLICATION DATA:
APPLICATION UNMBER: US/08/8:
FILING DATE: 03-APR-1997
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMEER: 08/643,219
APPLICATION UNMEER: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: CENTE OF APPLICATION:
                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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STRANDEDNESS: doub
TOPOLOGY: linear
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                                                                                                                                                                                                                    ZIP: 60064-3500
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                                                                                                                                                                                                                                                                                                  STREET:
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APPLICATION NUMBER:
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100 Abbott Park Road
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                                              UMBER: US/08/851,350
05-MAY-1997
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FILING DATE: ATTORNEY/AGENT INFORMATION:

5940.US.P2

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RESULT 15
US-09-132-154-12
US-09-132-154-12
; Sequence 12, Applicatio
; Patent No. 6251867
; Patent INFORMATION:
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SEQUENCE CHARACTERISTICS:
LENGTH: 2497 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                 CLASSIFICATION:
PRIOR APPLICATION NUMBER: US/08/832,08
APPLICATION NUMBER: US/08/832,08
FILING DATE: 03-APR-1997
APPLICATION NUMBER: 08/643,219
FILING DATE: 06-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: CASULO, Dianne
REGISTRATION NUMBER: 40,943
REFERENCE/DOCKET NUMBER: 5940.US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
TELEPHONE: 847-938-3137
INFORMATION FOR SEQ ID NO:
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REGIEVE 40,943
REFERENCE/DOCKET NUMBER: 59-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Davidson, Donald J.
TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ Version 2.0
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
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Local Similarity 85.0%;
hes 147; Conservative
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                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 60064
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                                                                                                      5940.US.P1
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Best Local Similarity 85.0%;
Matches 147; Conservative
                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 2497 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: cDNA
2032
                                                                       1972
                                                                                                                                        1912 CCACTGCTTGGAGAAGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA 1971
                          128 CACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
                                                                                         68 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC 127
                                                                                                                                                                      8 CCTCATCTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA
                                                                     AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC
CACACGAAAAGATATTGCCTTGCTAAAGCTAAGCAGTCCTGCCGTCATCACTG 2084
                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                   Score 132.6; DB Pred. No. 1e-35;
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Search completed: May 26, 2006, 13:54:15 Job time : 96 secs

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Minimum DB
Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                         Query
Match Length DB
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| EMC_Celerra_SIDSJ/ptodata/2/pubpna/US09_PUBCOMB.seq:*
| EMC_Celerra_SIDSJ/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
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| EMC_Celerra_SIDSJ/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
| EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
| EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
| EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
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| EMC_Celerra_SIDSJ/ptodata/2/pubpna/US10G_PUBCOMB.seq:*
| EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
| EMC_Celerra_SIDSJ/ptodata/2/pubpna/US11B_PUBCOMB.seq:*
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Listing first 45 summaries
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11 15 US-11-124-368A-8354
2 9 US-10-741-600-17618
2 10 US-10-95-561-13234
4 US-09-925-065A-869309
4 US-09-925-065A-869309
5 US-09-925-065A-869309
5 US-09-925-065A-86262
5 US-09-925-065A-869309
6 US-10-741-601-5650
10 US-10-995-561-13269
10 US-10-995-561-34448
10 US-10-995-561-34498
11 US-10-995-561-34498
12 US-10-741-600-6797
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Sequence 886252,
Sequence 869309,
Sequence 886262,
Sequence 13269, Ap
Sequence 13269, A
Sequence 9, Appli
Sequence 14344, A
Sequence 14349, A
Sequence 2896, Ap
Sequence 2896, Ap
Sequence 6797, Ap
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Sequence 25501, A
Sequence 8354, Ap
Sequence 17618, A
Sequence 13234, A
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ALIGNMENTS

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                   181
                                                    121 TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG
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GENERAL INFORMATION:

APPLICANT: CARGILL, Michele et al.

APPLICANT: CARGILL, Michele et al.

TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

TITLE OF INVENTION: DETECTION AND USES THEREOF

PILE REFERENCE: CL001559

CURRENT APPLICATION NUMBER: US/10/995,561

CURRENT FILING DATE: 2004-11-24

NUMBER OF SEQ ID NOS: 85702

SOFTWARE: FASUSEQ for Windows Version 4.0

SEQ ID NO 25501

LENGTH: 201

TYPE: DNA

ORGANISM: Homo saplens
                                                                                                                                                             TITLE OF INVENTION: Genetic Polymorphisms Associated with TITLE OF INVENTION: Vascular Diseases, Methods of Detection and FILE REFERENCE: CLO01524

CURRENT APPLICATION NUMBER: US/11/124,368A

CURRENT FILING DATE: 2005-05-09

PRIOR APPLICATION NUMBER: US 60/568,845

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-05-07

PRIOR FILING DATE: 2004-11-09

NUMBER OF SEQ ID NOS: 21112

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8354

LENGTH: 201

TYPE: DNA

ORGANISM: Homo sapiens

US-11-124-368A-8354
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US-11-124-368A-8354/c
; Sequence 8354, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
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                                                                               Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 201; Conservative 0
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                                                                               Score 200.6; DB 15;
Pred. No. 4.5e-61;
); Mismatches 0; I.
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Sequence 1334, Application US/1099561

Publication No. US20050272054A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: DETECTION AND USES THEREOF
TITLE OF INVENTION: DETECTION AND USES THEREOF
TILE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT APPLICATION NUMBER: US/11-24
NUMBER OF SEQ ID NOS: 85702
SOPTWARE: PASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17618, Application US/10741600

Publication No. US20050026169A1

GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001499

CURRENT APPLICATION UMBER: US/10/741,600

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 73997

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 17618

LENGTH: 93112

TYPE: DNA

CORDANTSM: 40mc Seriage
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Matches
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Pred. No. 5.6e-60;
Nismatches 0;
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human G
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 2000-11-30
PRIOR FILING DATE: 20001-01-05
PRIOR FILING DATE: 20001-01-05
PRIOR FILING DATE: 20001-01-05
PRIOR FILING DATE: 20001-05-09
NUMBER OF SEQ ID NOS: 957086
SECTION OF SEG FOR Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 5.6e-60;
Matches 201; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 869309
                                                                                                                                                                                                                                                                                                                                 LENGTH: 614
TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-869309
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Local Similarity 95.0%;
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| TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
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                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                   Score 187.4; DB 4; Length 614; Pred. No. 3.8e-56;
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; TYPE: DNA; ORGANISM: Homo sapiens US-09-925-065A-886262
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CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
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US-09-925-065A-886262/c
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Sequence 869309, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 886262
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
APPLICANT: Wang, David G.

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single TITLE OF INVENTION: Nucleotide Polymorphisms in the Huma FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-20
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/289,846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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Pred. No. 3.8e-56;
2; Mismatches 8
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APPLICATION NUMBER: US 60/250,092

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GENERAL INFORMATION: GENERAL INFORMATION: GENERAL INFORMATION: Identification and Mapping of Single TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/252,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR APPLICATION NUMBER: US 60/289,846
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PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FRENESEQ for Windows Version 4.0
SEQ ID NO 869309
LENGTH: 614
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; ORGANISM: Homo sapiens
US-09-925-065A-869309
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                                                                                                                                   Best Loc
Matches
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SEQ ID NO 886262
LENGTH: 614
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                                                                                                                                                                       Query Match
                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Homo sapiens
-09-925-065A-886262
                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 957086
                                                                                                                                                   Local Similarity
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CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT
                                                          TTGACRTCCTCATCTTTTCTAGGTCCCCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG
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95.0%;
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Pred. No. 3.8e-56;
                                                                                                                                   Score 187.4; DB 5;
Pred. No. 3.8e-56;
2; Mismatches 8;
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Sequence 5650, Application US/10741601
Publication No. US20040166519A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENERIC POLYMORPHISMS AS TITLE OF INVENTION: STENOSIS, METHODS OF DEFILE AFFERENCE: CLOO1500
CURRENT APPLICATION NUMBER: US/10/741,601
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 26415
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 5650
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US-10-995-561-13269
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US-10-741-601-5650
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                                                                  ; ORGANISM: Homo sapiens
US-10-995-561-13269
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                                                                                                                          GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILE REFERENCE: CL001559
CUGRENT APPLICATION NUMBER: US/10/995,561
CUGRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 13269
LENGTH: 63693
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Publication No. US20050272054A1
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Best Local Similarity 95.0%;
Matches 191; Conservative
Query Match
Best Local Similarity
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TYPE: DNA
                                                                                                                 TYPE: DNA
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    93.4%;
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Pred. No. 2.6e-55;
2; Mismatches 8;
    Score 187.4; DB 10;
Pred. No. 2.6e-55;
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RESULT 13

US-10-741-601-14344, Application US/10741601

; Sequence 14344, Application US/10741601

; Publication No. US20040166519A1

; PUBLICANT: CARGILL, Michele et al.
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001500

; CURRENT APPLICATION NUMBER: US/10/741,601

; CURRENT FILING DATE: 2003-12-22

; NUMBER OF SEQ ID NOS: 26415

; SOPTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Zaas, Aimee
APPLICANT: Schwartz, David A.
APPLICANT: Peltz, Gary
ITILE OF INVENTION: Polymorphic Plasminogen Ger
FILE REFERENCE: DUKE-09785;
CURRENT APPLICATION NUMBER: US/11/108,459
CURRENT FILING DATE: 2005-04-18
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9
CHENGTH: 52280
TYPE: DNA
ORGANISM: Homo sapiens
US-11-108-459-9
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US-11-108-459-9
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Publication No. US20060051780A1
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Best Local Similarity 95.0%;
Matches 191; Conservative
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US-10-741-601-14344
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US-10-995-561-34498
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US-11-124-368A-2896
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APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION: GENETIC POLYMOFHISMS ASSOCIATED WITH
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RES
TITLE OF INVENTION: DETECTION AND USES THEREOF
FILLE REFERENCE: CL001559
CURRENT APPLICATION NUMBER: US/10/995,561
CURRENT FILING DATE: 2004-11-24
NUMBER OF SEQ ID NOS: 85702
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 34498
LENGTH: 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 34498, Application US/10995561
Publication No. US20050272054A1
GENERAL INFORMATION:
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Best Local Similarity
                                                                      GENERAL INFORMATION:
                                                                                        Sequence 2896, Application US/11124368A Publication No. US20050287559A1
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Best Local 9
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TYPE: DNA
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177; Conserv
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Pred. No. 4.2e-51;
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Pred. No. 4.2e-51;
1; Mismatches 8
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APPLICANT: Michele Cargill APPLICANT: James J. Devli APPLICANT: May Luke

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APPLICANT: Manus J. Devlin
APPLICANT: May Luke
TITLE OF INVENTION: Genetic Polymorphisms Associated with
TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
FILE REFERENCE: CL001524
CURRENT APPLICATION NUMBER: US/11/124,368A
CURRENT FILING DATE: 2005-05-09
PRIOR APPLICATION NUMBER: US 60/568,845
PRIOR FILING DATE: 2004-05-07
PRIOR APPLICATION NUMBER: US 60/625,936
PRIOR FILING DATE: 2004-11-09
NUMBER OF SEQ ID NOS: 21112
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2896
LENGTH: 91561
TYPE: DNA
ORGANISM: Homo Bapiens
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                                                                                  Query Match 82.1%;
Best Local Similarity 98.0%;
Matches 197; Conservative
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LOCATION: 221, 222, 233, 2
LOCATION: 233, 234, 235, 2
LOCATION: 245, 246, 247, 2
OTHER INFORMATION: n = A,T
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LOCATION: 162, 163, 164, 1
LOCATION: 174, 175, 176, 1
LOCATION: 186, 187, 188, 1
LOCATION: 186, 187, 200, 2
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LOCATION: 115, 116, 117, 118, 11
LOCATION: 125, 129, 130, 11
LOCATION: 139, 140, 141, 142, 14
LOCATION: 139, 140, 141, 142, 14
LOCATION: 151, 152, 153, 154, 15
OTHER INFORMATION: n = A,T,C or
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LOCATION: 1, 2, 3, 4, 5, 6, 7,
LOCATION: 18, 19, 20, 21, 22, 2
LOCATION: 32, 33, 34, 35, 36, 3
LOCATION: 46, 47, 48, 49, 50, 5
LOCATION: 60
                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 256, 257, 258, 259, 260,
LOCATION: 268, 269, 270, 271, 272,
LOCATION: 280, 281, 282, 283, 284,
LOCATION: 292, 293, 294, 295, 296,
OTHER INFÖRMATION: n = A,T,C or G
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189, 190,
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154, 155,
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Search completed: May 26, 2006, 14:28:23 Job time: 855 secs
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                                                                   GTCTTCACCCCACGCTGGTGA 77873
                                                                                     GTCTTCACCCCACGCTGGTGA
                                                                                                                               TGGAGCCCACACAAGCAGATATTGCCTT-CTAAAGCTAAGCAGGTACTCGCTCACCTGTG 77852
                                                                                                                                                     TGGAGCCCACACAAGCAGATATTGCCTTGCTAAAGCTAAGCAGGTACTCGCTCACCTGTG 180
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November 2005

Published_Applications Mucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Mewly publications make up the Published Applications Main databases.

Searches run against Mucleic Acid Published_Applications produce two sets of results, with the extensions ... rnpbm (Published_Applications_NA_New):
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions ... rapbm (Published_Applications_AA_New).

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Result
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Maximum Match 100%
Listing first 45 summaries
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length: 2000000000
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| EMC_Celerra_SIDS3/ptodata/1/pubpna/US05_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US06_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US07_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
| EMC_Celerra_SIDS3/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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(without alignments)
986.511 Million cell updates/sec
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(c) 1993 - 2006 Biocceleration Ltd
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US-10-473-173-75
US-11-953-349-1537
US-11-953-349-11978
US-10-953-349-1516
US-10-953-349-15193
US-10-953-349-15193
US-10-953-349-15193
US-10-953-349-17913
US-11-217-529-79011
US-11-217-529-79011
US-11-217-529-7402
US-11-217-529-7602
US-11-217-529-7602
US-11-217-529-7607
US-11-217-529-7601
US-11-217-529-7601
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US-11-217-529-77601
US-11-217-529-77601
US-11-217-529-77601
US-10-953-349-11818
US-10-953-349-11818
US-11-217-529-3294
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US-11-217-529-3294
US-11-217-529-3294
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Sequence 11978, A
Sequence 19516, A
Sequence 3, Appli
Sequence 15193, A
Sequence 2815, Ap
Sequence 1913, Ap
Sequence 79011, A
Sequence 740, App
Sequence 740, App
Sequence 2493, Ap
Sequence 2767, App
Sequence 7601, A
Sequence 212, App
Sequence 212, App
Sequence 2180, A
Sequence 2193, Ap
Sequence 856, App
Sequence 856, App
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Sequence 15327, A
Sequence 471, App
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12.0	12.0	12.0	12.1	12.1	12.1	12.1	12.1	12.1	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.2	12.3	12.3	12.3
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US-10-473-173-334	US-10-473-173-296	US-11-217-529-173718	US-10-505-928-151	US-10-953-349-9734	US-10-953-349-11275	US-10-953-349-26846	US-10-953-349-2736	US-10-953-349-4870	US-11-217-529-786	US-10-196-749-347	US-11-293-697-942	US-10-953-349-939	US-10-953-349-39485	0-953-349-31	US-10-953-349-39//3	US-10-488-619-309	US-10-511-937-566	-11-293-697	US-11-217-529-1043
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ALIGNMENTS

á Ş 밁 S ; TYPE: DNA ; ORGANISM: Homo US-10-473-173-75 US-10-473-173-75 밁 APPLICANT: VAN AUNEL INSTITUTE APPLICANT: VAN AUNEL INSTITUTE TITLE OF INVENTION: Microarray Gene Expression Profiling in Clear Cell Renal Cell TITLE OF INVENTION: Carcinoma: Prognosis and Drug Target Identification FILE REFERENCE: 38345-170094 FILE REFERENCE: 38345-170094 CURRENT APPLICATION NUMBER: US/10/473,173 CURRENT FILING DATE: 2003-09-29 PRIOR APPLICATION NUMBER: US 60/279,411 PRIOR APPLICATION NUMBER: US 60/279,411 PRIOR PILING DATE: 2001-03-29 PRIOR PILING DATE: 2001-03-29 NUMBER OF SEQ ID NOS: 498 SOPTWARE: PatentIn version 3.2 SEQ ID NO 75 LENGTH: 2732 PRIOR Sequence 75, Application US/10473173 Publication No. US20060088823A1 GENERAL INFORMATION: Query Match Best Local Similarity Matches 147; Conserv 1977 1917 128 83 æ CACACAAGCAGATATTGCCTTAAAAGCTAAGCAGGTACTCGCTCACCTGTG 180 AGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCTTGGAGCC ccactgctriggagaagrecccaaggcctricarcctacaaggreatccrigggreeacacacca CCTCATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTGCACACCA CACACGAAAAGATATTGCCTTAAAAGCTAAGCAGTCCTGCCGTCATCACTG AGAAGTGAATCTCGAACCGCATGTTCAGGAAATAGAAGTGTCTAGGCTGTTCTTGGAGCC Conservative sapiens 66.1%; 85.0%; Score 132.6; DB Pred. No. 2e-36; Mismatches DB 6; 25; Length 2732; <u>,</u> Gaps 1976 127 67

RESULT 2
US-10-953-349-15327
US-10-953-349-15327; Application US/10953349
; Sequence 15327, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
 TITLE OF INVENTION: ENCONDED THERBY
 PILE REFERENCE: 2750-1579082

CURRENT APPLICATION NUMBER: US/10/953,349

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GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/20/203-28
NUMBER OF SEQ ID NOS: 5458
SOPTWARE: PATENTIN VET: 2.1
SEQ ID NO 471
LENGTH: 3038
TYPE: DNA
ORGANISM: Homo sapiens
US-11-293-697-471
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; ORGANISM: Glycine max
US-10-953-349-15327
SEQ ID NO 11978
                                                                                                                                                                       Sequence 11978, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version
SEQ ID NO 15327
            APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT PILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PACENCIN Version 3.3
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Local Similarity 53.6%;
                                                                                                                                                                                                                                                                                                                                                     154 AGCTAAGCA 162
                                                                                                                                                                                                                                                                                                                                                                                         564 GTACCAAAGTÁGTGTATGAGGTGCGCTCAGGAGGCÁCCGTÁGTÁGAAAATGGAGTGCACÁ 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     504 CTACATCTACCATTGGCCCAGAGGGGGTCCATCAGAAAGGAGTCAAAGTCTATGATGATG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109 CTAGGCTGTTCTTGGAGCCCACACAGAGATATTGCCTTGCTAAAGCTAAG 160
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40252
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; Pred. No. 2.6;
1; Mismatches
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Pred. No. 0.27;
1; Mismatches
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; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-11978
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE:
TITLE OF INVENTION: ENCOUNED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SECTION NO 19516
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
                                                                                                 SOFTWARE: FASTSE
SEQ ID NO 3
LENGTH: 394191
                                                                                                                                                                           Sequence 3, Application US/10506549

Publication No. US20060100417A1

GENERAL INFORMATION:

APPLICANT: APPLERA CORPORATION

TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,

TITLE OF INVENTION: AND USES THEREOF

FILE REFERENCE: CL001361-US

CURRENT APPLICATION NUMBER: US/10/506,549

CURRENT FILING DATE: 2004-09-03

PRIOR APPLICATION NUMBER: 60/361,343

PRIOR FILING DATE: 2002-03-05

NUMBER: SECO. TO NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                              ORGANISM: Homo
                                                                                  TYPE: DNA
NAME/KEY: misc_feature
LOCATION: (1)...(394191)
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57; Conserv
                                                                                                                                              FastSEQ for Windows Version
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52.8%;
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Pred. No. 1.9;
1; Mismatches

    Mismatches

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Pred. No. 1.
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Sequence 9738, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRA-
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: Patentin version 3.3
SEQ ID NO 9738
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                                                                                                                                     ; LENGTH: 3420
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9738
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; ORGANISM: Glycine max
US-10-953-349-15193
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US-10-953-349-15193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ) OTHER INFORMATION: n = US-10-506-549-3
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Publication No. US20060107345A1
GENERAL INFORMATION:
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
TILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PALEBRIN VERSION 3.3
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Best Local
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Local Similarity 47.0%;
les 78; Conservari
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Local Similarity 71.4%;
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51 ATCCTGGGTGCACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATTRGAAGTGTCT 110
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51; Conser
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                                                          Score 26.4; DB 6;
Pred. No. 8.3;
1; Mismatches 42;
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Pred. No. 50;
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APPLICANT: Morris, MacDonald
APPLICANT: Rosenberg, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
FILE REFERENCE: 506612000104
CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: US 10/31,831
PRIOR APPLICATION NUMBER: US 10/31,831
PRIOR APPLICATION NUMBER: US 10/31,831
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 10/325,899
PRIOR FILING DATE: 2002-12-20
NUMBER OF SEO ID NOS: 3117
SOFTWARE: PATENTIN VERSION 3.2
1 FENCTH: 6050
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US-10-511-937-2815/c
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US-11-293-697-1913/c
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                                                                                                                                                                                                                                                Sequence 1913, Application US/11293697 Publication No. US20060105376A1 GENERAL INFORMATION:
                 SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1913
LENGTH: 3059
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                                                                           APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: Novel full length cDNA FILE REFERENCE: HI-A0106 CURRENT APPLICATION NUMBER: US/11/293,697 CURRENT FILING DATE: 2005-12-05 PRIOR APPLICATION NUMBER: US/10/108,260 PRIOR FILING DATE: 2002-03-28 NUMBER OF SEQ ID NOS: 5458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                          385
                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCTGTTCT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TIGAÇATCCTÇATCTTTTCTAGGTCCTCAAGGCCTTCATCCTACAAGGTCATCCTGGGTG
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Woodward, Robert
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Morris, MacDonald
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Pred. No. 11
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US-11-217-529-76402/c
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PRIOR PILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
SOFTWARE: Patentin version 3.3
SEQ ID NO 79011
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                                                                                                                                                                                                                                                                                                  Sequence 76402, Application US/11217529 Publication No. US20060099612A1
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              CURRENT APPLICATION NUMBER: US/11/217,529
CURRENT FILING DATE: 2005-09-02
PRIOR APPLICATION NUMBER: US 10/932,182
PRIOR FILING DATE: 2004-09-02
NUMBER OF SEQ ID NOS: 197023
                                                                                                                                    APPLICANT: SUNTORY LIMITED
APPLICANT: NAKAO, YOSHIHIRO
APPLICANT: NAKAO, YOSHIHISA
APPLICANT: NAKAYURA, NORIHISA
APPLICANT: KODAWA, YUKIKO
APPLICANT: KODAWA, YUKIKO
APPLICANT: FUJIMURA, TOMOKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
APPLICANT: ASHIKARI, TOSHIHIKO
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SOFTWARE: PatentIn version 3.3
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CURRENT FILING DATE: 2005-09-02
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APPLICANT: ASHIKARI, TOSHIHIKO
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: S-38-285
                                                                                                                       FILE REFERENCE: S-38-285
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Local Similarity 51.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56 GGGTGCACACCAAGAAGTGAACCTCGAATCTCATGTTCAGGAAATRGAAGTGTCTAGGCT 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGATGCÁGAANACGAGTGGAÁTGTGGÁÁANATTCANANÁGGACTTCGÁÁGTCAATÁTTTC 134
                                                                                                                                                                                                                                                                                                                                                                                                                             GTCATTAGACGCAAGAGAGACAAATTTCGACTTGATAAA 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAKAMURA, NORIHISA
KODAMA, YUKIKO
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53.5%;
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Pred. No. 11;
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  Best Local Similarity
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RESULT 13
US-11-293-697-740/c
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                                                                                                                            ÚS-10-488-619-2493
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US-11-293-697-740
                                                                                                                                                                                                                                  APPLICANT: Greenlee, Winner and Sullivan, P.C.

APPLICANT: Greenlee, Winner and Sullivan, P.C.

TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Association:

TITLE OF INVENTION: Physiological Conditions, And Genotyping Arrays

FILE REFERENCE: 98-01 WO

CURRENT APPLICATION NUMBER: US/10/488,619

CURRENT FILING DATE: 2004-03-01

NUMBER OF SEQ ID NOS: 3040

SOFTWARE: Patentin version 3.1

SEQ ID NO 2493

LENGTH: 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2493, Application US/10488619 Publication No. US20060099578A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 740, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
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LENGTH: 1734
                               Query Match
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Best Local
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TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: HI-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 26
TYPE: DNA
                                                                                                                                                           ORGANISM: Mus musculus
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ilarity 54.3%;
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Pred. No. 19;
0; Mismatches
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Pred. No. 1
Score 25;
Pred. No.
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                                       Length 631;
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Sequence 226, Application US/10505928

| Publication No. US20060088532A1
| Publication No. US20060088532A1
| GENERAL INFORMATION:
| APPLICANT: Ludwig Institute for Cancer Research et al.
| TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
| FILE REFERENCE: 28967/39178
| CURRENT APPLICATION NUMBER: US/10/505,928
| CURRENT FILING DATE: 2004-08-27
| PRIOR APPLICATION NUMBER: US 60/363,019
| PRIOR FILING DATE: 2002-03-07
| NUMBER OF SEQ ID NOS: 866
| SOFTWARE: Patentin 3.2
| SEQ ID NO 226
| LENGTH: 4908
| TYPE: DNA
| ORGANISM: Homo sapiens
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Search completed: May 26, 2006, 14:28:53 Job time: 25 secs
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                                                                                                                         148 TGCTAAA 154
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                                                                                    TGCAACA 1145
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